

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.0526 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKSLRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	400	1 JCI428	ketol-acid reducto
2	1508.5	72.3	395	1 A24709	ketol-acid reducto
3	1494.5	71.6	404	2 T40532	ketol-acid reducto
4	497	23.8	333	2 F70407	acetohydroxy acid
5	486	23.3	332	2 H75044	ketol-acid reducto
6	484.5	23.2	331	2 AC1694	ketol-acid reducto
7	483	23.2	342	2 C69644	ketol-acid reducto
8	480.5	23.0	331	2 AB1323	ketol-acid reducto
9	469.5	22.5	581	2 T06825	ketol-acid reducto
10	465	22.3	591	1 S30145	ketol-acid reducto
11	465	22.3	591	2 T45681	ketol-acid reducto
12	463	22.2	335	2 C90204	ketol-acid reducto
13	463	22.2	337	2 A96911	ketol-acid reducto
14	459.5	22.0	340	2 C84032	ketol-acid reducto
15	458.5	22.0	336	2 D72362	ketol-acid reducto
16	456	21.9	331	2 AD2095	ketol-acid reducto
17	450	21.6	348	1 F64492	ketol-acid reducto
18	444	21.3	367	1 A47037	ketol-acid reducto
19	442.5	21.2	334	2 F89997	ketol-acid reducto
20	438.5	21.0	595	1 S17180	alpha-keto-beta-hy
21	432.5	20.7	336	2 G95051	ketol-acid reducto
22	432.5	20.7	340	2 C97922	ketol-acid reducto
23	429	20.6	363	2 C75387	ketol-acid reducto
24	427.5	20.5	337	2 C81801	ketol-acid reducto
25	427.5	20.5	337	2 F81066	ketol-acid reducto
26	415	19.9	340	2 B86778	ketol-acid reducto
27	414.5	19.9	332	2 H69497	ketol-acid reducto
28	409	19.6	344	1 S35140	probable ketol-aci
29	405.5	19.4	333	2 A69059	ketol-acid reducto

30	405	19.4	340	2 G81411	ketol-acid reducto
31	393	18.8	338	2 E83059	ketol-acid reducto
32	387	18.6	338	1 C48648	ketol-acid reducto
33	381	18.3	366	2 E82634	ketol-acid reducto
34	378	18.1	332	2 T35830	acetolactate synth
35	360	17.3	333	1 JC5166	ketol-acid reducto
36	349	16.7	333	2 H87120	ketol-acid reducto
37	349	16.7	343	2 T45415	ketol-acid reducto
38	340	16.3	333	2 D70855	probable ilvC prot
39	335	16.1	339	2 G87511	ketol-acid reducto
40	329.5	15.8	339	2 AB3330	ketol-acid reducto
41	329	15.8	330	1 B64561	ketol-acid reducto
42	329	15.8	339	2 AE2824	ketol-acid reducto
43	329	15.8	339	2 D97602	hypothetical prote
44	325	15.6	330	2 A71945	ketol-acid reducto
45	321	15.4	491	1 ISECKR	ketol-acid reducto

ALIGNMENTS

RESULT 1

JCI428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N/Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
C/Species: Neurospora crassa
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C/Accession: JCI428
R/Siata-H.-Bowman, B.

(Gene 120, 115-118, 1992)

A/Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-be
A/Reference number: JCI428; MUID:93013010; PMID:1398116
A/Accession: JCI428
A/Molecule type: DNA
A/Residues: 1-400 <SIS>
A/Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:G168821; PIDN:1
C/Genetics:
A/Map position: V
A/Introns: 68/1; 78/3; 170/3; 392/3
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F/87-273/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 100.0%; Score 2086; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.9e-146;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQVRGVKTMDF 60

Db 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQVRGVKTMDF 60

QY 61 GHKEEVEHVRADYPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGLNIVGVKNGKSW 120

Db 61 GHKEEVEHVRADYPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGLNIVGVKNGKSW 120

QY 121 EDALQDQWPGKKNLFDVDEAISRGITVMNLLSDAAQSETWPHIKPOITTKGKTLFYSHGFS 180

Db 121 EDALQDQWPGKKNLFDVDEAISRGITVMNLLSDAAQSETWPHIKPOITTKGKTLFYSHGFS 180

QY 181 PVFKDLTKVEVPTDNDVILVAPKSGRTVRSILFREGGINSSPAVYQDVTGKAKEKAV 240

Db 181 PVFKDLTKVEVPTDNDVILVAPKSGRTVRSILFREGGINSSPAVYQDVTGKAKEKAV 240

QY 241 GVAVSGGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSPAFN 300

Db 241 GVAVSGGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSPAFN 300

QY 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 360

Db 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 360

QY 361 SLEYNQPDYRERYEAELEIRNLEIWRAGKSLRPENQK 400

C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C/Accession: F70407
F:/Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: F70407
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-333 <AQF>
A/Cross-references: UNIPROT:O67289; UNIPARC:UPI0000056582; GB:AEO00730; NID:g2983674; PT:
A/Experimental source: strain VF5
C/Genetics:
A/Gene: ilvC
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase
F:/21-203/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.8%; Score 497; DB 2; Length 333;
Best Local Similarity 34.7%; Pred.No. 4.6e-29;
Matches 115; Conservative 70; Mismatches 124; Indels 22; Gaps 9;

Qy 78 LDYFKNDTLALIGYSQGCGGLNRDNGLNVLIVGVKNKGSWEDATQDGWVGKMLFDV 137
Db :
12 LDIILDKVIALIGYSQGCGHAHALNLRDSGLNVILGHEGSRREKAKADF---EVTYP 67
Qy 138 DEAIRSGTIVNNLLSDAAQSSTPH-IKPQITKGKLTLYFSHGSPVPKDLTKVEVPTDV 196
Db :
68 REAAKRADIIMFLPDTVQPEVKYNEVEPELNSKTLAFAGHFNHPRIQP--PKDVD 124
Qy 197 VIIVAPKSGRTVRSLEPRGGINSSFAVDYTGRAKEKAVALGVAVGS--GYLYETTF 254
Db :
125 VFWVAPKPGHLVWMVTTEGKGPVALVIHQDASGTCKKALAYAKGIGATRAGVIETTF 184
Qy 255 EKEYSYDLYGERGCMGCIHGMFLAQVEYLERGRHSSEAFNETVBEATOSLYPLIGAHG 314
Db :
185 KEETETDLFGEMVLCGGVITALIKAGFELVNAGYQPEVAYFECLHE-LKLIVDLLIEHG 243
Qy 315 MDWMFDCASTTARRGAIDWTTPKFDALKVPNNLYDSVKNGBDRKRSLEYN--SQPDY-- 370
Db :
244 ISGMRYGISDTAKYGVDVTRGERIYKVVKPVMEKTLEIQGEPAREWILENKAGRPPVYA 303
Qy 371 ---RER---YEAEIDLEIRNLEIWRAGKSLR 395
Db :
304 LLERDREHLVEKVEELURKMPW-LGKKELK 333

RESULT 5
H75044
ketol-acid reductoisomerase (ilvC) PAB0889 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C/Accession: H75044
R/anonymouse, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A/Reference number: A75001
A/Accession: H75044
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-332 <KAW>
A/Cross-references: UNIPROT:Q9U0Z9; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID:
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: ilvC; PAB0889
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase
F:/24-206/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.3%; Score 486; DB 2; Length 332;
Best Local Similarity 37.8%; Pred.No. 3e-28;
Matches 122; Conservative 63; Mismatches 120; Indels 18; Gaps 9;

QY 355 GDERKRSLEYNQPDYRERYEAELDEI 381
Db 297 GFKEFHMRKEQQGHQIEKVGAELREM 323

RESULT 7
C69644
ketol-acid reductoisomerase ilvC - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
A:Accession: C69644
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erttington, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maunda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:198044033; PMID:9384377
A:Accession: C69644
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <KUN>
A:Cross-references: UNIPROT:P37253; UNIPARC:UPI00000398DER; GB:Z99118; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
F;21-202/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.2%; Score 483; DB 2; Length 342;
Best Local Similarity 38.3%; Pred. No. 5.2e-28;
Matches 119; Conservative 58; Mismatches 108; Indels 26; Gaps 10;

QY 80 YPKND-----TLALIGYSGQGHGQGLNRDNGNLNIVGVKNGKSWEDAIDQGWVP 130
Db 5 YNGDITKENVLAKTVAVIGYSGQGHGQGLNRDNGNLNIVGVKNGKSWEDAIDQGWVP 130

QY 131 GKPLFDVDEAISRTGTVNMLLSDAQSETW-PHIKQITKGKTLVPSHGFSVPFKDLTKV 189
Db 60 GHKVFVSKEAAQAIEIIVLLPDEQOQKYEAIEKDELTAGKSLVFAHGFNVHFQIVP- 118

QY 190 EVPTDVIDVLVAPKSGRTVRSFLFREGGINSFVAYQDVTKAKEKAVAGVAVG---S 246
Db 119 --PADVDVFLVAPKSGRLVRRTYEQAGVGFALFAIYQDVTKAKEKAVAGVAVG 176

QY 247 GYLTYETFEKVEYSDLYGREGCLMGHGMFLAQYVLRERHSPSEAFNETVEEATQSL 306
Db 177 GVL-ETTFKEETDLDLFGQAVLCGGSALVAGFETLVEAGYQPELAYFECLHE-LKLI 234

QY 307 YPLIGAHGMDWMPDACSTTARRGAIDWTPKFKDA-LKPVFNLLYDSVKNGDKRSKSLYN 365
Db 235 VDLWVEEGLAGMRYISIDTAQWGDVFGSGPRVVDKAYKESMKVLDIQNGTFKAWIVEN 294

QY 366 SQDDYRERYEA 376
Db 295 QV--NRPRFNA 303

RESULT 8
AB1323
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004

C:Accession: AB1323
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <GLA>
A:Cross-references: UNIPARC:UPI0000054PF8; GB:NC_003210; PIDN:CAD00064.1; PID:gl6411439;
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
Query Match 23.0%; Score 480.5; DB 2; Length 331;
Best Local Similarity 37.9%; Pred. No. 7.5e-28;
Matches 124; Conservative 52; Mismatches 116; Indels 35; Gaps 10;

QY 79 DYFKND-----TLALIGYSGQGHGQGLNRDNGNLNIVGVKNGKSWEDAIDQGWVP 133
Db 8 DAVKNNALGKTVAVIGYSGQGHGQGLNRDNGNLNIVGVKNGKSWEDAIDQGWVP 62

QY 134 LFDVDEAISRTGTVNMLLSDAQSETWPH-IKPIQITKGKTLVPSHGFSVPFKDLTKVEVP 192
Db 63 VYSVSEADKADVIWLLPDETQETYEIEIKPNLKAGNSLVFAHGFNIHF---DVINFP 119

QY 193 TDVDVLVAPKSGRTVRSFLFREGGINSFVAYQDVTKAKEKAV--ALGVAVGSGYLY 250
Db 120 SDVDVFLVAPKSGRLVRRTYEQAGVGFALFAIYQDVTKAKEKAV--ALGVAVGSGYLY 179

QY 251 ETTTFKEVEYSDLYGREGCLMGHGMFLAQYVLRERHSPSEAFNETVEEATQSLYPLI 310
Db 180 ETTTFKEETDLDLFGQAVLCGATHLIQAGFETLVEAGYQPELAYFEVLHE-MKLI 238

QY 311 GAHGMWMPDACSTTARRGAIDW-----TPFKDALKVPFNNL-----YDSVKN 354
Db 239 YEGGKRSLEYNQPDYRERYEAELDEI 381

QY 355 GDERKRSLEYNQPDYRERYEAELDEI 381
Db 297 GFKEFHMRKEQQGHQIEKVGAELREM 323

RESULT 9
T06825
ketol-acid reductoisomerase (EC 1.1.1.86) - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C:Accession: T06825
R:Zhu, X.
Submitted to the EMBL Data Library, August 1998
A:Reference number: Z15837
A:Accession: T06825
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-591 <ZHU>
A:Cross-references: UNIPROT:O82043; UNIPARC:UPI000012DS26; EMBL:Y17796; PIDN:CAA76854.1
A:Experimental source: cv. G2
C:Genetics:
A:Gene: pgaair
C:Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol
C:Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;113-311/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.5%; Score 469.5; DB 2; Length 581;
Best Local Similarity 26.8%; Pred. No. 1.1e-26;
Matches 140; Conservative 62; Mismatches 128; Indels 193; Gaps 10;

QY 1 MAA--RNCTKALRPLAROLATP-----AVORTFVAASAVRASVAV 40
DB 1 MAATVSSCTAISASCKTAKPVAASAPFTNLSPKLSQSIARRRSITVGSALGAT--- 57
QY 41 KAAAPARQOVRGVKTMDF-----AGHKEEYHERADWPAEKLLDYFKN-DTLA 87
DB 58 KVSAPPATHPV-----SLDFETSVPKKERVNLGAGHEEYVIRGRDLPHLLPDAFKGIQIG 113
QY 88 LIGYSQGHGQGLNLRD-----NGLNIVGVKRGKSNEDAIQDGVWPGK-NLFDVDEA 140
DB 114 VIGWSQGPQAQNLRLSLVEAKSDIVVKVGLRKGSSSFNEAREAGFSEKGTGLGDIWET 173
QY 141 ISRGITVNNLLSDAAQSTWPHIKPQITKTKLYFSHGSPFVKDLTKVVEPTDVLV 200
DB 174 ISGDLVLLLSDSQAADNYEKIFSHLKPNSILGLSHQSLGSLGKPNFNVIAV 233
QY 201 APKSGRTVRSFLRGR-----GINSSPANYQDVTGKAKAKAVAGVAVGSLYETTFE 255
DB 234 CPKMGPSVRLYVQKKEINGAGINSFVGHQDVGRTATNVALGWSVALGSPFTFATLE 293
QY 256 KEVTSDDLGERGCLMGHIG----- 275
DB 294 QEYKSDIFGERGILLGAVHGVESLFRYRYTENGMSDLAYKNTVESITGVISTQGM 353
QY 276 ----- 275
DB 354 LAVYNALSEDGKBFKAYSASFYPCMEILYECYEDVASGSEIRSVVLGRFRFYKEGLP 413
QY 276 -----MFLAQEVLRLRERHSPSEA 294
DB 414 APFMKIDQTRMKVGERVSTRPAGDLGLPYPTAGVVFAMMAQIEVLKKGHSYSEI 473
QY 295 FNETVEATOSLYPLIGHGMDWMDACSTTARRGAIDWTPKF 337
DB 474 INESVIESVDSLNFPMHARGVSFVMDNCSTTARLGSRKWAPRF 516
RESULT 10
S30145
ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana
N/Alternate names: acetohydroxy acid isomeroeductase
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004
C/Accession: S30145; S34040; S36884
R/Curien, G.; Dumas, R.; Douce, R.
A/Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy ac
A/Reference number: S30145; MUID:93192533; PMID:8448371
A/Accession: S30145
A/Molecule type: mRNA
A/Residues: 1-591 <CUR>
A/Cross-references: UNIPROT:Q05758; UNIPARC:UPI0000171F83; EMBL:X68150
submitted to the EMBL Data Library, July 1992
A/Reference number: S34040
A/Accession: S34040
A/Molecule type: mRNA
A/Residues: 1-284, 'R', 286-591 <DUM>
A/Cross-references: UNIPARC:UPI000016DB78; EMBL:X68150; NID:g288062; PIDN:CAA48253.1; PI
R/Dumas, R.; Curien, G.; DeRose, R.T.; Douce, R.
Biochem. J. 294, 821-828, 1993
A/Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and charact
s thaliana (thale cress).
A/Reference number: S36884; MUID:93393563; PMID:8379936
A/Accession: S36884
A/Molecule type: DNA
A/Residues: 1-578, 'A', 580-591 <DU2>
A/Cross-references: UNIPARC:UPI0000000A7B; EMBL:X69880; NID:g402551; PIDN:CAA49506.1; PI
C/Genetics:
A/Genome: nuclear
A/Introns: 99/3; 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
C/Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase hom
C/Keywords: chloroplast; isoleucine-valine biosynthesis; isomerase; oxidoreductase

F:1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:68-591/Product: ketol-acid reductoisomerase #status predicted <MAT>
F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.3%; Score 465; DB 1; Length 591;
Best Local Similarity 27.2%; Pred. No. 2.3e-26;
Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;

QY 7 TKALRPLARQLATPAVQRTFVAASAVRASVAVKA-VAAPARQOVRGVKTMDFAGHKEE 65
DB 44 SKLSRLT---ATVAGNGATGSSLAARWSSAVKAPVSLDFETSVFKKVKSLAGVEEY 100
QY 66 VHERADWPAEKLLDYFKN-DTLALIGYSQGHGQGLNLRD-----NGLNIVGVKRGK 118
DB 101 IVRGSRDLFKHLPDPAFKGIQKIGVIGWSQGPQAQNLRLSLVEAKSDIVVKIGLRKGR 160
QY 119 SWEDIAQDGVV-PGKNLFDVDEALSRGTIVNNLLSDAAQSTWPHIKPQITKTKLYFSH 177
DB 161 SFPEARAGFTESGTLGDIWETIAGSDVLILLISDAQAADNYEKIFSHMKPNLSILGLSH 220
QY 178 GFSPVFKDLTKVEVPTDVLVAPKSGRTVRSFLRGR-----GINSSFAVYQDVTGK 232
DB 221 GFLGLHQLSSGLDFPKNISVAVCPKMGPSVRLYVQKKEINGAGINAFVAVHVDVGR 280
QY 233 AKKAVAGVAVGSLYETTFEYVSDLYGRCGLMGHIG----- 275
DB 281 AADVAGWSVALGSPFTFATTLQEVRSDFGERGILLGAVHGVESLFRYRYTENGMSD 340
QY 276 ----- 275
DB 341 LAYKNTVECTGTISRTISQGLMAYVNSLSBEGKDFETAYSASFYPCMEILYECYEDV 400
QY 276 ----- 275
DB 401 QSGSEIRSVVLGRFRFYKEGLPAFPMGNIDQTRMKVGERVRSRPAAGDLGLPYPTAG 460
QY 276 -----MFLAQEVLRLRERHSPSEAFTNETVEATOSLYPLIGHGMDWMDACSTTARRGAI 331
DB 461 VYVALMAAQIEILRKGHSYSEINESVIESVDSLNPFPFHARGVSFVMDNCSTTARLGSR 520
QY 332 DWTPKF 337
DB 521 KWAPRF 526

RESULT 11

T45681

ketol-acid reductoisomerase - Arabidopsis thaliana

N/Alternate names: protein F14P22.200

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 05-Oct-2004

C/Accession: T45681

R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;

submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23011

A/Accession: T45681

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-591 <DAN>

A/Cross-references: UNIPROT:Q05758; UNIPARC:UPI0000000A7B; EMBL:AL137082

A/Experimental source: cultivar Columbia; BAC clone F14P22

C/Genetics:

A/Map position: 3

A/Introns: 99/3; 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3

A/Note: F14P22.200

C/Superfamily: Ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol

F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match

22.3%; Score 465; DB 2; Length 591;

Best Local Similarity 27.2%; Pred. No. 2.3e-26;

Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;

QY 7 TKALRPLARQLATPAVQRTFVAASAVRASVAVKA-VAAPARQOVRGVKTMDFAGHKEE 65

Db 44 SKLSRST---ATVAGNGATGSLAARMVSSSAVKAPVSLDFTSVFKKESVLAGEY 100
Qy 66 VHERADWPAEKLDYFKN-DTALIGYSGHGGQGLNLRD-----NGLNVIIVGRKNGK 118
Db 101 IVRGDRDLFKHLPDAFKGIQIGVIGSGGQPAQAQNLRDSLVEAKSDIVVKLGKRGSR 160
Qy 119 SWEDATQDQHW-FGKNLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSH 177
Db 161 SPEEARAAGFTESGTLGDIWETIAGSDLVLLISDAAQADNVEKIFSHMKPNSILGLSH 220
Qy 178 GFSVPFKDLTKVEVPDQDVLVAPKSGGTVRSLSFREG------GINSFAYQDVTK 232
Db 221 GFLGLHLSQGLDFPKNISVAVCPKMGSGSVRLVYQKGKEINGAGINASFVHQDVDR 280
Qy 233 AKKAVAGVAVSGYLYETTFEKEVYSDLYGRGCLMGGIHG----- 275
Db 281 AADVALGWSVALGSPPTFATLLEQYRSDFIGERGILLGNVHGIVESLFRYTYENGMSD 340
Qy 276 ----- 275
Db 341 LAYKNTVECTITRTISTRTISQGLAVVNSLSEGGKDFETAVSFPQMEILYECYEDV 400
Qy 276 ----- 275
Db 401 QSGSEIRSVVLAGRRFYKEGLPAFPNGNIDQTRMMKVGRVRSKSPAGDGLPLYPFTAG 460
Qy 276 ----MFLAQEVLRERGHSPSEAFNETVEATOSLYPLICAHGMDWDFACSTTARRGAI 331
Db 461 VYVALMMAQIEILRKKGHSSEIINSESVIESVDLSNPFHEARGVSPWVNCSTIARLGR 520
Qy 332 DWTPKF 337
Db 521 KWAPRF 526
RESULT 12
C90204
ketol-acid reductoisomerase (ilvC-1) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C:Accession: C90204
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90204
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KUR>
A:Cross-references: UNIPROT:Q9UWX9; UNIPARC:UPI000012D50D; GB:AE006641; NID:g13813740; E
C:Genetics:
A:Gene: ilvC-1
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
Query Match 22.2%; Score 463; DB 2; Length 335;
Best Local Similarity 34.1%; Pred. No. 1.5e-26;
Matches 112; Conservative 55; Mismatches 115; Indels 46; Gaps 8;
Qy 78 LDYFKNDTLALIGYSGHGGQGLNLRDGLNVIIVGRKNGKSWEDAIQDGVPGKVLFDV 137
Db 15 LDLIKGRITAVLGYSQGRAWAQNLRDGLNVIIVGLEREGKSWELAKSDGITP----LHT 70
Qy 138 DEAISRGITVIMNLLSDAAQSETW-PHIKPOITKGTLYFSHSGSPVFKDLTKVEVPTD 196
Db 71 KDAVKDADIIIFVPMVQKTLWLESVQPMKKGADLVFAHGFNIHYK---LIDPPKDS 127
Qy 197 VILVAPKSGRTVRSLFREGRGINSFAYQDVTKAKKAVAGVAVGS--GYLYETTF 254
Db 128 VYMIAPKPGPTREYKAGGVPALVAHQDVSGTALHKALAIKAGIGATRAGVPTTF 187

Qy 255 EKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATOSLYPLIGANG 314
Db 188 KEETETDLFGEQVILVGGIMELMRAAFETLVEGQPEVAYPETINE-LKMLVDLVYKXG 246
Qy 315 MDWMPDCASTTARRG-----AIDWTPKFDALKPVF 345
Db 247 ISGMLKAVSDTAKYGGMTVGVKVIDESVVRKMKALQRIKSGKFAEWEVEYGRGMPVV 306
Qy 346 NNLYDSVKNGBDK-----RSLEYNSQP 368
Db 307 NGL-SNVQNSLEEKIGNQLRDLVQKGP 333
RESULT 13
A96911
ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C:Accession: A96911
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96911
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <KUR>
A:Cross-references: UNIPROT:Q97WV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0091
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
Query Match 22.2%; Score 463; DB 2; Length 337;
Best Local Similarity 35.2%; Pred. No. 1.5e-26;
Matches 118; Conservative 62; Mismatches 135; Indels 20; Gaps 9;
Qy 64 EBVHERADWPAEKLDYFKNDTLALIGYSGHGGQGLNLRDGLNVIIVGRKNGKSWEDA 123
Db 2 EELKYVYDEAD--LNYLKDKKIIAIGFSGQGHAAHLNKLKESGLNVIIVGLYDGSKSKVA 59
Qy 124 IQDGVPGKNLFDVDEAISRGITVIMNLLSDAAQSETW-PHIKPOITKGTLYFSHGFSPV 182
Db 60 EDYGF----EYEVADAVKQAOVVMILLPDEKQKQIYEASIKDNLDEGDLFFAHGFNIH 115
Qy 183 FKDLTKVEVPTDQDVLVAPKSGGTVRSLSFREGINSFAYQDVTKAKKAVAGV 242
Db 116 YNQIVP---PRNVDVMTAPKGPGHIVRRQYTEGGVPCLYAVHQDYTGKKEIALAYGK 172
Qy 243 AVG--SGLYYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 300
Db 173 GIGGTGKGVMTTTFKTIETETDLFGQAVLCGGICALINAGYDTLREAGYSAENAYFECFH 232
Qy 301 EATQSLYPLIGAHGMDWMPDCASTTARRG-AIDWTPKFDALKPVFNILYDSVKNGBDK 359
Db 233 E-MKMLVDLVYGGMGMAKRYISIDTAEYGDYVVGVRNLINDNVRAEMKKVLTBIQDTFAK 291
Qy 360 RSLEYN--SQPDYRERYAEELDEIRNLRIWRAGR 392
Db 292 NWLLENQTRPAFNARRIHDR----ETEKVGR 322
RESULT 14
K84032
ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession: C84032
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 20.7895 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-2
Perfect score: 2071
Sequence: 1 MLRTQARLLCNSRVITAKR.....RNMEIWKVGEVRKLRPENO 395

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 80:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	1 A24709	ketol-acid reducto
2	1508.5	72.8	400	1 UC1428	ketol-acid reducto
3	1467.5	70.9	404	1 T40532	ketol-acid reducto
4	495	23.9	332	2 H75044	ketol-acid reducto
5	485.5	23.4	333	2 H70407	ketol-acid reducto
6	478	23.1	348	1 F64492	ketol-acid reducto
7	470	22.7	337	2 A96911	ketol-acid reducto
8	468	22.6	331	2 A21694	ketol-acid reducto
9	468	22.6	335	2 C92024	ketol-acid reducto
10	468	22.6	336	2 D72362	ketol-acid reducto
11	461	22.5	331	2 AB1323	ketol-acid reducto
12	461	22.3	342	2 C69644	ketol-acid reducto
13	443.5	21.4	340	2 C84032	ketol-acid reducto
14	442	21.3	367	1 A47037	ketol-acid reducto
15	441.5	21.3	334	2 F89997	ketol-acid reducto
16	437	21.1	363	2 C75387	ketol-acid reducto
17	435.5	21.0	591	1 S30145	ketol-acid reducto
18	435.5	21.0	591	2 T45681	ketol-acid reducto
19	435.5	20.9	337	2 C81801	ketol-acid reducto
20	433.5	20.9	337	2 F81066	ketol-acid reducto
21	433.5	20.9	581	2 T06825	ketol-acid reducto
22	432.5	20.9	331	2 A69059	ketol-acid reducto
23	432	20.8	331	2 AD2095	ketol-acid reducto
24	431	20.8	340	2 C97922	ketol-acid reducto
25	428.5	20.7	336	2 G95051	ketol-acid reducto
26	421.5	20.4	332	2 H69497	ketol-acid reducto
27	397	19.2	595	1 S17180	ketol-acid reducto
28	394	19.0	340	2 B86778	ketol-acid reducto
29	389	18.8	366	2 B82634	ketol-acid reducto

30	385	18.6	340	2 G81411	ketol-acid reducto
31	372.5	18.0	344	1 S35140	probable ketol-aci
32	369	17.8	332	2 T35830	acetolactate synth
33	365	17.6	338	2 E83059	ketol-acid reducto
34	359.5	17.4	338	1 C48648	ketol-acid reducto
35	357	17.2	333	1 JC5166	ketol-acid reducto
36	352.5	17.0	339	2 AB3330	ketol-acid reducto
37	350.5	16.9	339	2 AE2824	ketol-acid reducto
38	350.5	16.9	339	2 D97602	hypothetical prote
39	339	16.4	491	1 ISECKR	ketol-acid reducto
40	339	16.4	491	2 D91217	ketol-acid reducto
41	339	16.4	491	2 E86063	ketol-acid reducto
42	336	16.2	333	2 D70855	probable ilvC prot
43	336	16.2	333	2 H87120	ketol-acid reducto
44	336	16.2	343	2 T45415	ketol-acid reducto
45	335	16.2	492	2 AG0473	ketol-acid reducto

ALIGNMENTS

RESULT 1
A24709 ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: acetohydroxyacid reductoisomerase ILV5; protein L9638.7; protein YLR33;
C:Species: Saccharomyces cerevisiae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A24709, S51463
R:Peteren J.G.L.; Holmberg S.
Molecular Acids Res. 14, 9631-9651, 1986
A:Title: The ILV5 gene of *Saccharomyces cerevisiae* is highly expressed.
A:Reference number: A24709; MUID:87117524; PMID:3027658
A:Accession: A24709
A:Molecule type: DNA
A:Residues: 1-395 <PEP>
A:Cross-references: UNIPROT:P06168; UNIPARC:UP1000012D529; EMBL:X04969; NID:G3826; PIDN:C;
R:Du, Z.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of *S. cerevisiae* coamid 9638.
A:Reference number: S51459
A:Accession: S51463
A:Molecule type: DNA
A:Residues: 1-395 <DUZ>
A:Cross-references: UNIPARC:UP1000012D529; EMBL:U19102; NID:G609396; PIDN:AA867753.1; PII
C:Genetic:8;
A:Gene: SGD:ILV5, MIPS:YLR355C
A:Cross-references: SGD:S0004347; MIPS:YLR355C
A:Map position: 12R
C:Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
F:81-267//Domain: ketol-acid reductoisomerase homology <KAR>
Query Match 100.0%; Score 2071; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTQARLLCNSRVITAKRTPALATPAALYSPRAAFVPMITTRRLKQINRGTYETV 60
Db 1 MLRTQARLLCNSRVITAKRTPALATPAALYSPRAAFVPMITTRRLKQINRGTYETV 60
QY 61 YERADMPREKLDYFKNDTPALIGYSGQYGQGLNLDNGNLVIGYKXGASAKAIED 120
Db 61 YERADMPREKLDYFKNDTPALIGYSGQYGQGLNLDNGNLVIGYKXGASAKAIED 120
QY 121 GWVPGKULFTVEDAIKRGSYVMNLSDAQSETPAIKPLLTGKTLTFSHGSPVVKDL 180
Db 121 GWVPGKULFTVEDAIKRGSYVMNLSDAQSETPAIKPLLTGKTLTFSHGSPVVKDL 180
QY 181 THVEPPKDLVILVAPGSGRTVRSLEKRGGINSSAYVNDVTGKAHEKQALAAVIGS 240
Db 181 THVEPPKDLVILVAPGSGRTVRSLEKRGGINSSAYVNDVTGKAHEKQALAAVIGS 240
QY 241 GYVYQTFPERVNSDLGEGRCIMGIGHMFLAQYDVLRENGHSPBAFVETVETATQSL 300

```
Db      241 GYAYQTFEEFVNSDLGEGCIMGHGMFLAQYDLRNGHSPSEAFMEVEEAQSL 300
Qy      301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKRSLEFNS 360
Db      301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKRSLEFNS 360
Qy      361 QPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395
Db      361 QPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395
```

RESULT 2

```
UC1428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N/Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
C/Species: Neurospora crassa
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C/Accession: UC1428
R/Sister, H.; Bowman, B.
Gene 120, 115-118, 1992
A/Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-
A/Reference number: UC1428; MUID:3013010; PMID:1398116
A/Accession: JCI428
A/Molecule type: DNA
A/Residues: 1-400 <SIS>
A/Cross-references: UNIPROT:P38674; UNIPARC:UP1000012D525; GB:M84189; NID:G168821; PIDN:
C/Genetics:
A/Map position: 11V-2
A/Intons: 68/1, 78/3, 170/3, 392/3
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F/87-273/Boman: ketol-acid reductoisomerase homology <KAR>
```

```
Query Match      72.8%; Score 1508.5; DB 1; Length 400;
Best Local Similarity 73.6%; Pred. No. 2.1e-105;
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;
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Qy      4 TQARILCNSRVITAA--KRTF---ALATRAA---AYSPPARFVKMITTRGLKQINFG 54
Db      7 TKLRPLARGLATPAPVQRRTFVAASAVRASVAKVAARQOV-----RGVKIMDFA 60
Qy      55 GTVETVYERADWPREKLDLDFKNDFTALIGYSQGYGGGGLNDGMLNVIIGVKDGASW 114
Db      61 GHKEEYVERADWPAEKLDLDFKNDFTALLIGYSQGYGGGGLNDGMLNVIIGVKDKGSW 120
Qy      115 KAILEDGWVPGKULFTVEDAIKRGSYVMNLSDAOSETWPAIKPLLTGKTLTFSGHGS 174
Db      121 EDALIDGWVPGKULFDVDAISRGITVMNLLSDAOSETWPHIKPOLTKGTLTFSGHGS 180
Qy      175 PVFKDLTHVEPPKDLVILVAPKSGRTVRSLEFKEGRGINSYAVWMDVTGKAHEKAQAL 234
Db      181 PVFKDLTHVEPPKDLVILVAPKSGRTVRSLEFKEGRGINSYAVWMDVTGKAHEKAQAL 240
Qy      235 AVAIGSGYVQTFEERFVNSDLYGERGCLMGHGMFLAQYDLRNGHSPSEAFMEVE 294
Db      241 GVAVGSGYVLETTFEKEVYSDLYGERGCLMGHGMFLAQYDLRNGHSPSEAFMEVE 300
Qy      295 EAQOSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKR 354
Db      301 EAQOSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKR 360
Qy      355 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395
Db      361 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 399
```

```
RESULT 3
T40532
ketol-acid reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomy
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
```

```
C/Accession: T40532; T43303; T42540
R/Purnille, B.; Goffeau, A.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A/Reference number: Z21935
A/Accession: T40532
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-404 <PUR>
A/Cross-references: UNIPROT:P78827; UNIPARC:UP1000012D527; EMBL:AL023288; NID:G5832408; I
A/Experimental source: strain 972h-; cosmid c56F2
R/Kawamukai, M.
submitted to the EMBL Data Library, December 1997
A/Description: S.pombe ILVs homolog.
A/Reference number: Z22407
A/Accession: T43303
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 262-404 <KAW>
A/Cross-references: UNIPARC:UP10000168765; EMBL:AB09603; NID:G2696653; PIDN:BAA24000.1;
R/Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A/Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A/Reference number: Z17323; MUID:98162722; PMID:9501991
A/Accession: T42540
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-37; 'R', 39-40, 'W', 42-91, 'S', 93-237, 'T', 239-274, 'P', 276-296, 'P', 298-393, 'G',
A/Cross-references: UNIPARC:UP1000016909E; EMBL:D89175; NID:G1749557; PIDN:BAI1837.1; PJ
C/Experimental source: strain PR745
C/Genetics:
A/Map position: 2
A/Map position: 2
A/Pathway: branched-chain amino acid biosynthesis
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F/88-274/Domin: ketol-acid reductoisomerase homology <KAR>
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Query Match      70.9%; Score 1467.5; DB 2; Length 404;
Best Local Similarity 70.2%; Pred. No. 2.5e-102;
Matches 276; Conservative 48; Mismatches 64; Indels 5; Gaps 1;
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Qy      2 LRTQARILCNSRVITAKRTFALATPAAYSRPARFVKMITTRGLKQINFGTETVY 61
Db      14 LRTMSGR-----FLATRSMSVWARITAAAPSMFAPRMTAPLMQTRGMRVMDFAGTENW 68
Qy      62 ERADWPREKLDLDFKNDFTALIGYSQGYGGGGLNDGMLNVIIGVKDGASWKAIEDG 121
Db      69 ERADWPREKLDLDFKNDFTALIGYSQGYGGGGLNDGMLNVIIGVKDGASWKAIEDG 128
Qy      122 WVPKULFTVEDAIKRGSYVMNLSDAOSETWPAIKPLLTGKTLTFSGHGSFVKDLT 181
Db      129 WVPKULFTVEDAIKRGSYVMNLSDAOSETWPAIKPLLTGKTLTFSGHGSFVKDLT 188
Qy      182 HVEPPKDLVILVAPKSGRTVRSLEFKEGRGINSYAVWMDVTGKAHEKAQALVAGSG 241
Db      189 KHPPKDLVILVAPKSGRTVRSLEFKEGRGINSYAVWMDVTGKAHEKAQALVAGSG 248
Qy      242 YVYQTFEERFVNSDLYGERGCLMGHGMFLAQYDLRNGHSPSEAFMEVEEAQSLY 301
Db      249 YVYQTFEERFVNSDLYGERGCLMGHGMFLAQYDLRNGHSPSEAFMEVEEAQSLY 308
Qy      302 PLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKRSLEFNSQ 361
Db      309 PLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFODLYESTNGTETKRSLEFNSQ 368
Qy      362 PDYREKLEKELDTIRNMEIWKVGEVYKRLRPEN 394
Db      369 PDYREKLEKELDTIRNMEIWKVGEVYKRLRPEN 401
```

```
RESULT 4
H75044
```


QY 361 QPDYREKLEKELDTIRNME-----IMVKYGEVRKL 390
| : : : : :
| : : : : :
Db 313 -----REAGFPNMLRLREKELHLEKVKELRKM 342

RESULT 7

A/Accession: A96911
A/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C/Accession: A96911
R/Nolling, U.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: A96911
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-337 <KUR>
A/Cross-references: UNIPROT:Q97MV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1;
A/Experimental source: Clostridium acetobutylicum ATCC824
A/Genetic8: CAC0091
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom

Query Match 22.7%; Score 470; DB 2; Length 337;
Best Local Similarity 36.1%; Pred. No. 1.1e-27;
Matches 122; Conservative 56; Mismatches 130; Indels 28; Gaps 10;

QY 72 LDYFKNDTFALLIGYSGQYGGGLNRDNGNLNIIIGVRKDGASWKALEDGWVPGKMLFTV 131
| : : : : :
| : : : : :
Db 14 LNTLKDKKIALIGSGQGHAAHLNLRKESGLNVIIGLYDGSKSWKVAEDYGF----EYVEV 69

QY 132 EDALIKGGSYVMNLSDAQSFTWPA-IRPLTKGKTLVPSHGSPVVKDLTHVBPDKLD 130
| : : : : :
| : : : : :
Db 70 ADANRQAVVWMLLPDRKQRIYEASIKMDLDEBDALFFAHGFRINHQIV---PPKQVD 126

QY 191 VIIVAPGSGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQALAVAI--SGVYQTTF 248
| : : : : :
| : : : : :
Db 127 VMLAIAPGPHIYRQRTTBEGGVPCLYAVQDITGKKEIALYAGKIGTGKGMWMTTF 186

QY 249 EREVNDSLYGERGCLMGHGMFLAQYDLRENGHSPSEAFNETVEATOSLYPLIGKYG 308
| : : : : :
| : : : : :
Db 187 KIETETDLFGEQAVLCGGLCALINAGYDLREAGYSKNAVFEQPHH-MQMTVDLWYEGG 245

QY 309 MDVWYDCACTTARRGALDWY---PIFKNALKPVFDLYESTKNGTETKSLERN--SQPD 363
| : : : : :
| : : : : :
Db 246 MAKRRYSISDTAEYG--DYVVGNRLLINDNVAEKKKVLTREIODGTFAKNWMLLENQGRPA 303

QY 364 YREKLEKELDTIRNMEIMVKYGEVRKL-----RPENQ 395
| : : : : :
| : : : : :
Db 304 FNARRRLEAD---REIEKVKKRLRGMSWINENPSNE 337

RESULT 8

AC1694
ketol-acid reductoisomerase (acetohydroxy-acid isomeroeductase) homolog ilvC [imported]
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C/Accession: AC1694
R/Glaeser, P.; Fisinger, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A/Authors: Krefit, U.; Kuhn, M.; Kunst, F.; Kurepkat, G.; Madeno, E.; Maltournam, A.; Maok, C.; Schleuter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A./Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1694
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-331 <GLA>
A/Cross-references: UNIPARC:UPI00000CC759; GB:AL592022; PIDN:CAC97323.1; PID:G16414607; C
A/Experimental source: strain C1p11262
C/Genetic8:
A/Genetic: ilvC
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom

Query Match 22.6%; Score 468; DB 2; Length 331;
Best Local Similarity 37.3%; Pred. No. 1.6e-27;
Matches 125; Conservative 60; Mismatches 118; Indels 32; Gaps 13;

QY 73 DYKND-----TPALLIGYSGQYGGGLNRDNGNLNIIIGVRKDGASWKALEDGWVPGKMLFTV 127
| : : : : :
| : : : : :
Db 8 DAVKNNALRGKTAIVIGYSGQGHAAHLNLRKESGLNVIIGLYDGSKSWKVAEDYGF----EYVEV 62

QY 128 LDFVDAIRKGSYVMNLSDAQSFTWPA-IRPLTKGKTLVPSHGSPVVKDLTHVBPDKLD 186
| : : : : :
| : : : : :
Db 63 VIVSEAEKADYVIMLLPDRKQRIYEASIKMDLDEBDALFFAHGFRINHQIV---PPKQVD 119

QY 187 KDLVILVAPKSGGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQALAVAI--SGVYQTTF 244
| : : : : :
| : : : : :
Db 120 SDVDVFLVAPKSGGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQALAVAI--SGVYQTTF 179

QY 245 QTTFERVNSDLYGERGCLMGHGMFLAQYDLRENGHSPSEAFNETVEATOSLYPLIGKYG 304
| : : : : :
| : : : : :
Db 180 ETTFKETETDLFGEQAVLCGGLCALINAGYDLREAGYSKNAVFEQPHH-MQMTVDLWYEGG 238

QY 305 GKXGMDVWYDCACTTARRGALDWY---PIFKNALKPVFDLYESTKNGTETKSLERN--SQPD 363
| : : : : :
| : : : : :
Db 239 YEGGMKMHSHSNTAEYDYGVPVVDYADTKKAKVELTTL---QNGNFAKSFIDN 294

QY 360 SQPDYRE--KLEKELDTIRNMEIMVKYGEVRKL 392
| : : : : :
| : : : : :
Db 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 295 KN-GFKEPFRMRKEQ---QHQIEKVGKRLRMRMP 325

QY 249 EREVNSDLYGERGCLMGHGMFLAQVDVLRNGHSPSEAFNTEVEATQSLYPLICKY 308
 Db 188 KEETETDIFGEQVILVIGGIMELMRAAFTLVBEQGFVAYETITNE-LKMLVDLVYK 246
 QY 309 MDVYDASTTARRGALDWYP-IFKNALKPVFQDIYESTKNGTEKRSLEFNSQDYREK 367
 Db 247 ISGMLKAVSDIKYGMVYGVKVIDESVRKKMKALQRIKSKFAEWEV-----EYGRG 301
 QY 368 LE---KEIDTIRNMEIWKVEKVRKL 390
 Db 302 MPTVNVGNLSNVQNSLEKIGNQLRL 327
 RESULT 10
 D72362
 C:Species: Thermotoga maritima (strain MSB8)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
 C:Accession: D72362
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A12200; PMID:99287316; PMID:10360571
 A:Accession: D72362
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-336 <ARN>
 A:Cross-references: UNIPROT:Q9WZ20, UNIPARC:UP1000012D560, GB:AE001730, GB:AE000512, NID
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0550
 C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
 F:21-203/Domain: ketol-acid reductoisomerase homology <KAR>
 Query Match 22.6%; Score 468; DB 2; Length 336;
 Best Local Similarity 35.6%; Pred. No. 1.6e-27;
 Matches 117; Conservative 66; Mismatches 124; Indels 22; Gaps 8;
 QY 72 LDYFKNDFALIGYSGYGGGLNRDNGLVNITIGVRKDGASWKAIEDGMVPGKMLTFV 131
 Db 12 LNLIDKKRIAIIGYSQGHANLNKDGSLNVVGLRSGSKWKAEBQ---GLTVKTI 67
 QY 132 BDALIRGSGYVNNLSDAQSSETWPA-IRPLLTGKTLVFSGFSVPFVDLTHVEPKD 190
 Db 68 BEAAKEADITIMLLPDERHOPETIKYIEKHLTEGMLFAHGFNHQIT---PPKVD 124
 QY 191 VILVAPKSGRTVRSILFKRGINSYAVMNDVTGSKAHEKAQALVAIG--SGVYVQTF 248
 Db 125 VTMIAFKSPGHIVREYVGRVPLVAVYQDTGKADIALAYKGIQVTRAGIETTF 184
 QY 249 EREVNSDLYGERGCLMGHGMFLAQVDVLRNGHSPSEAFNTEVEATQSLYPLICKY 308
 Db 188 KEETETDIFGEQVILVIGGIMELMRAAFTLVBEQGFVAYETITNE-LKMLVDLVYK 246
 QY 309 MDVYDASTTARRGALDWYP-IFKNALKPVFQDIYESTKNGTEKRSLEFNSQDYREK 367
 Db 247 ISGMLKAVSDIKYGMVYGVKVIDESVRKKMKALQRIKSKFAEWEV-----EYGRG 301
 QY 368 LE---KEIDTIRNMEIWKVEKVRKL 390
 Db 302 MPTVNVGNLSNVQNSLEKIGNQLRL 327
 RESULT 11
 AB1323
 ketol-acid reductoisomerase (acetohydroxy-acid isomeroeductase) homolog ilvc [imported]
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AB1323
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
 ; Dominguez-Bernal, G.; Duclaud, E.; Durand, L.; Dussange, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kunz, M.; Kunst, F.; Kurapat, G.; Madeno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; PMID:21537279; PMID:11679669
 A:Accession: AB1323
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-331 <GLA>
 A:Cross-references: UNIPARC:UP10000054F8; GB:NC_003210; PIDD:CAD00064.1; PID:gl6411439;
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: ilvc
 C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
 Query Match 22.5%; Score 465; DB 2; Length 331;
 Best Local Similarity 37.3%; Pred. No. 2.6e-27;
 Matches 125; Conservative 59; Mismatches 119; Indels 32; Gaps 13;
 QY 73 DYFKNDFALIGYSGYGGGLNRDNGLVNITIGVRKDGASWKAIEDGMVPGK 127
 Db 8 DAYNNALKEGTVAVIGYSGGHANLNKDGSLNVVGLRSGSKWKAEBQ---D 62
 QY 128 LFTVEDAIKRGSYVNNLSDAQSSETWPA-IRPLLTGKTLVFSGFSVPFVDLTHVEPP 186
 Db 63 VYSVSEADKADVIMILLPDETQETYEIEKPLKAGNSLVAFHGFNIHF-DV--INP 119
 QY 187 KDVLVILVAPKSGRTVRSILFKRGINSYAVMNDVTGSKAHEKAQALVAIG--GYV 244
 Db 120 SDVVFVLPAPGPHILVTRFTVEGAVPSLFAIYQDAGNARDPLASVAKIGTRAGVI 179
 QY 245 OTTEREVNSDLYGERGCLMGHGMFLAQVDVLRNGHSPSEAFNTEVEATQSLYPLI 304
 Db 180 EITKEETDIFGEQVILVIGGIMELMRAAFTLVBEQGFVAYETITNE-LKMLVDLVYK 246
 QY 305 GKYGDVYDASTTARRGALDWYP-IFKNALKPVFQDIYESTKNGTEKRSLEFNSQ 359
 Db 239 YEGEMKMRHSINSTAYEGDVSGRVVLTDTKKAMEVLTDI---QNGMFASFINDN 294
 QY 360 SQPDYRE--KLEKELDTIRNMEIWKVEKVRKL 392
 Db 295 KN-GFKEFHRRKQ---QGHQIEKVALREMP 325
 RESULT 12
 C69644
 ketol-acid reductoisomerase ilvc - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 C:Accession: C69644
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertek
 C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmerich, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidis, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
 Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelie,
 Rieger, M.; Rivolet, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsstra, E.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipal, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; PMID:98044033; PMID:9384377
 A:Accession: C69644
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-342 <KNA>
 A:Cross-references: UNIPROT:P37253; UNIPARC:UP10000038DEF; GB:Z59118; GB:AL009126; NID:94
 A:Experimental source: strain 168

Db 300 PRIVATEKAMRQILDEIQSGQFAREFVLNQAGKPGFTAMRRESEEL---IEEVGK 355

[illegible]

QY 386 EVRKL 390
Db 356 DLRAM 360

RESULT 15

89997
alpha-keto-beta-hydroxylacid reductoisomerase [imported] - Staphylococcus aureus (strain
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C:Accession: F89997
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:Cross-references: UNIPARC:UPI00000D7826; GB:BA000018; PID:g13701851; PIDN:BA043143.1;
A:Experimental source: strain N315
C:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom

Query Match 21.3%; Score 441.5; DB 2; Length 334;

Best local similarity 34.1%; Pred. No. 1.5e-25;

Matches 118; Conservative 68; Mismatches 125; Indels 35; Gaps 13;

QY 59 TVYERADMPREKLDYFKNDFALIGSGOGYGGCLNRDNGLANVIGVRKDGASWKAII 118
Db 3 TVY-----YDQVKTDLAQGKIAYGVYGSQGHANQNLKNDNGYDVVIGIR-PGRSFDKAK 57
QY 119 EDGAVPGKALFTVEDAIRGSIYVNLISDAAGSRTWP-AIKPLTKGKTLVESHGSPFVF 177
Db 58 EDGF----DVFPVAEAVKQADIVIVLTPDEIQGDVYKNEIEBNLEKHNALAFAGFNTHF 113
QY 178 KDLTHVEPPKDLVILVAPKSGRTVRSLFKEGRGINSYAVMNDVTGAHKAQALVA 237
Db 114 --GVIQPPADVDFLAPKGPGLVRRTPFEGSAVPSLFGIQDASQARNIALSYAKG 170
QY 238 IGS--GYVYQTFPEREVNSDLVYGERGCLMGHGFLLAQYDVLRENGHSPSEAFNEVTEB 295
Db 171 IGATPAGVIEFTTKEETETDLFGEQAVLCGVSKLIQSGFETVYAGYQPELAYFEVLHE 230
QY 296 ATQSLYPLIGKYGMDYWDACSTTARRGALDPT-----PIFKNALPVPQDLYESTKN 348
Db 231 -MKLIVDLMEGGMENVYSISNFAFG--DYVSGPRVITPDVKENMKAVLTLDI----QN 283
QY 349 GTETKRSLEFNSQPPYRE--KLEKELDTIRNKEIKVGEVRKLAP 392
Db 284 GNFSNRFTEDNKN-GFKEFYKLREBQ--HGHQIEKVGRELDREMP 325

Search completed: March 22, 2006, 15:34:33
Job time : 21.7895 secs

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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: March 22, 2006, 15:21:02 ; Search time 115.529 Seconds
 (without alignments)
 1528.885 Million cell updates/sec
 Title: US-10-797-248A-1
 Perfect score: 2094
 Sequence: 1 MSARGFSKALPMAQLATP.....EIMRAGKAVSLRPENQKQ 402
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2443163 seqs, 439378781 residues
 Total number of hits satisfying chosen parameters: 2443163
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A Geneseq 21.*
 1: Geneseqp1980s.*
 2: Geneseqp1990s.*
 3: Geneseqp2000s.*
 4: Geneseqp2001s.*
 5: Geneseqp2002s.*
 6: Geneseqp2003as.*
 7: Geneseqp2003bs.*
 8: Geneseqp2004s.*
 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2094	100.0	402	6	ABR64303
2	2081	99.4	400	6	ABR64306
3	2081	99.4	400	9	ADVL6807
4	1856	88.6	400	6	ABR64305
5	1671	79.8	403	9	ADVL6810
6	1668	79.7	396	6	ABJ26477
7	1668	79.7	508	6	ABJ26502
8	1634	78.0	388	6	ABJ25902
9	1634	78.0	500	6	ABJ25877
10	1526.5	72.9	400	4	AAU15089
11	1526.5	72.9	400	5	ABP73238
12	1503	71.8	395	6	ABR64304
13	1503	71.8	395	7	ADK64188
14	1421.5	67.9	409	7	ADB70124
15	1100.5	52.6	347	6	ABU20976
16	490	23.4	342	4	AAU01250
17	475	22.7	331	5	ABBA48168
18	475	22.7	331	6	ABU32456
19	473	22.6	332	4	AAB96356
20	472	22.5	337	6	ABU24174
21	469.5	22.4	336	6	ABU18526
22	468	22.3	579	2	AAV26183
23	468	22.3	579	2	AAV26180
24	468	22.3	585	8	ADX93651

SUMMARIES

ALIGNMENTS

RESULT 1

ABR64303
 ID ABR64303 standard; protein; 402 AA.
 XX.
 AC ABR64303;
 XX
 DT 16-SEP-2003 (first entry)
 XX
 DE Acetohydroxyacid isomeroreductase #1.
 XX
 KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
 XX
 OS Magnaporthe grisea.
 XX
 PN FR2829363-A1.
 XX
 PD 14-MAR-2003.
 XX
 PF 10-SEP-2001; 2001FR-00011689.
 XX
 PR 10-SEP-2001; 2001FR-00011689.
 XX
 PA (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 WPI; 2003-405775/39.
 XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
 PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroreductase.
 XX
 PS Claim 2; Fig 1; 66pp; French.
 XX
 CC The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (I) of acetohydroxyacid
 CC isomeroreductase. (I) are used for curative or preventative treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
 CC to illustrate the invention
 XX
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2094; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.4e-191;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Adx88429 Plant ful
 Ady07198 Plant ful
 Ady07344 Plant ful
 Adx77584 Plant ful
 Asg35210 Zea mays
 Asg35209 Zea mays
 Aau37780 Streptoco
 Aau38003 Streptoco
 Abu08004 S. pneumo
 AbU45897 protein e
 Adk47367 Streptoco
 Adr94886 Novel S.
 Aea58756 Streptoco
 Ady61069 Abiotic s
 Adm26226 Hyperther
 Agv04361 Plant ful
 Agv07450 Plant ful
 Adx92449 Plant ful
 Ady07435 Plant ful
 Aay26182 Soybean a
 Aag81458 S. epider

25 468 22.3 586 8 ADX88429
 26 468 22.3 588 8 ADY07198
 27 468 22.3 590 8 ADY07344
 28 468 22.3 590 8 ADX77584
 29 467 22.3 579 3 AAG35210
 30 467 22.3 596 3 AAG35209
 31 462.5 22.1 340 4 AAU37780
 32 462.5 22.1 340 4 AAU38003
 33 462.5 22.1 340 6 ABU08004
 34 462.5 22.1 340 6 ABU45897
 35 462.5 22.1 340 8 ADK47367
 36 462.5 22.1 351 8 ADR94886
 37 462.5 22.1 351 9 AEA58756
 38 462 22.1 581 9 ADY61069
 39 461.5 22.0 326 7 ADM26226
 40 458 21.9 571 8 ADY04361
 41 457 21.8 568 8 ADY07450
 42 457 21.8 578 8 ADX92449
 43 457 21.8 626 8 ADY07435
 44 452 21.6 586 2 AAY26182
 45 451.5 21.6 334 4 AAG81458

Qy	1	MSARGFSKALRPNARQLATPAVQRSFVAAASWVRATRKAAVAPTQQOIRGVKTMDFAGH	60
Db	1	MSARGFSKALRPNARQLATPAVQRSFVAAASWVRATRKAAVAPTQQOIRGVKTMDFAGH	60
Qy	61	KEQWVERADWPKEKLLLEYFKDUTLALIGVSGHGQGLNRDNGLNVLIGVRKDGKSWKD	120
Db	61	KEQWVERADWPKEKLLLEYFKDUTLALIGVSGHGQGLNRDNGLNVLIGVRKDGKSWKD	120
Qy	121	AVQDGVWPGKNLFEVDEAISRGTIVMNLISDAAQSETWPALKPQITKGKTLYFSHGFSVP	180
Db	121	AVQDGVWPGKNLFEVDEAISRGTIVMNLISDAAQSETWPALKPQITKGKTLYFSHGFSVP	180
Qy	181	FKDLTKVEVPTDQVDVILCAPKGGSGRTVRSLFREGRGINSFPVYQDVTGSAEKAIALGV	240
Db	181	FKDLTKVEVPTDQVDVILCAPKGGSGRTVRSLFREGRGINSFPVYQDVTGSAEKAIALGV	240
Qy	241	AIGSGYLKTTTPEKEVYSDLYGERCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA	300
Db	241	AIGSGYLKTTTPEKEVYSDLYGERCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA	300
Qy	301	TQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKEVFNQLYDSVKDGSSETQRSI	360
Db	301	TQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKEVFNQLYDSVKDGSSETQRSI	360
Qy	361	DYNSQPDYREKYEAEEMEEIRNLEIWRAGKAVRSRLENQOK	402
Db	361	DYNSQPDYREKYEAEEMEEIRNLEIWRAGKAVRSRLENQOK	402
RESULT 2			
ID	ABR64306	standard; protein; 400 AA.	
AC	ABR64306;		
DT	16-SEP-2003	(first entry)	
DE	Acetohydroxyacid isomeroreductas #2.		
XX	Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.		
XX	Magnaporthe grisea.		
XX	FR2829363-A1.		
XX	14-MAR-2003.		
XX	10-SEP-2001; 2001FR-00011689.		
XX	10-SEP-2001; 2001FR-00011689.		
XX	(AVET) AVENTIS CROPS SCIENCE SA.		
XX	Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;		
XX	WPI; 2003-405775/39.		
XX	N-PSDB; ACC80185, ACC80186.		
XX	Treatment of crops, useful for controlling fungi on, e.g. cereals,		
XX	potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid		
XX	isomeroreductase.		
XX	Disclosure; Page 57-58; 66pp; French.		
XX	The present invention relates to a method for controlling fungal disease		
XX	in crops by applying an inhibitor (I) of acetohydroxyacid		
XX	isomeroreductase. (I) are used for curative or preventative treatment of		
XX	a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or		
XX	rape. The present invention is an acetohydroxyacid isomeroreductase, used		
XX	to illustrate the invention		
XX	Sequence 400 AA;		

Query Match	99.4%;	Score 2081;	DB 6;	Length 400;
Best Local Similarity	99.8%;	Pred. No. 2.5e-190;		
Matches 399;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSARGFSKALRPMPAROLATPAVORESFVAASSMVRATRKAAVAPTOQOIRGVKTKMDPAGH	60	
Db	1	MSARGFSKALRPMPAROLATPAVQRTTFVAASSMVRATRKAAVAPTOQOIRGVKTKMDPAGH	60	
Qy	61	KEQVWERADWPKEKLLEYFKDDTLALICYGSGQGHGGLNLDNGNLNVIIGYRKDGSKSWKD	120	
Db	61	KEQVWERADWPKEKLLEYFKDDTLALICYGSGQGHGGLNLDNGNLNVIIGYRKDGSKSWKD	120	
Qy	121	AVDQGWPGKNLFEVDEAISRGTIVIMLLSDAAQSETWPALKPQITKGKTIYFSGHGFSPV	180	
Db	121	AVDQGWPGKNLFEVDEAISRGTIVIMLLSDAAQSETWPALKPQITKGKTIYFSGHGFSPV	180	
Qy	181	FKDLTKVEVPTDNDVIIICAPKSGSRTVRSLPREGRGINSSFAVYQDVTGGEAEKAIALGV	240	
Db	181	FKDLTKVEVPTDNDVIIICAPKSGSRTVRSLPREGRGINSSFAVYQDVTGGEAEKAIALGV	240	
Qy	241	AIGSGYLYKTTTFEKEVYSDLYGBRGCLMGGITHGMFLAQYEVLRERGHSPSEAFNETVBEA	300	
Db	241	AIGSGYLYKTTTFEKEVYSDLYGBRGCLMGGITHGMFLAQYEVLRERGHSPSEAFNETVBEA	300	
Qy	301	TQSLYPLIGANGMDWMYEAACSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDGSQTSQSL	360	
Db	301	TQSLYPLIGANGMDWMYEAACSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDGSQTSQSL	360	
Qy	361	DYNSQPDYREKYEAEMEIRNLEITWRAGKAVRSLRPENQK	400	
Db	361	DYNSQPDYREKYEAEMEIRNLEITWRAGKAVRSLRPENQK	400	
RESULT 3				
ADV16807				
ID	ADV16807	standard; protein; 400 AA.		
XX				
AC	ADV16807;			
XX				
DT	24-FEB-2005	(first entry)		
XX				
DE	M grisea ketol-acid reductoisomerase ILV5 seqid 6.			
XX				
KW	substrate inhibition; antibiotic; gene disruption;			
KW	ketol-acid reductoisomerase; ILV5; enzyme.			
XX				
OS	Magnaporthe grisea.			
XX				
FN	WO2004104176-A2.			
XX				
PD	02-DEC-2004.			
XX				
PF	17-MAY-2004; 2004WO-US015404.			
XX				
PR	15-MAY-2003; 2003US-0470947P.			
PR	19-MAY-2003; 2003US-0471615P.			
PR	21-MAY-2003; 2003US-0472242P.			
XX				
PA	(PARA-) PARADIGM GENETICS INC.			
PI				
PI	Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;			
PI	Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger RW;			
PI	Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;			
XX				
DR	WPI; 2005-021202/02.			
DR	N-PSDB; ADV16805, ADV16806.			
XX				
PT	Identifying a test compound as a candidate for an antibiotic comprises			
PT	contacting ornithine carbamoyltransferase (OCTase) or ketol-acid			
PT	reductoisomerase polypeptide, or fungal pathogenicity-conferring gene			
XX	with a test compound.			
PS	Claim 48; SEQ ID NO 6; 179pp; English.			

XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (Ocrase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting Ocrase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
 CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
 XX
 SQ Sequence 400 AA;

Query Match 99.4%; Score 2081; DB 9; Length 400;
 Best Local Similarity 99.8%; Pred. No. 2.5e-130;
 Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRATRKAAVAPTOQOIRGVKTMDFAGH 60
 DB 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRATRKAAVAPTOQOIRGVKTMDFAGH 60
 QY 61 KEQVWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSWKD 120
 DB 61 KEQVWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSWKD 120
 QY 121 AVQDQGWPGKMLFEVDIAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSHGSPV 180
 DB 121 AVQDQGWPGKMLFEVDIAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSHGSPV 180
 QY 181 FKDLTKVEVPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEEKAIALGV 240
 DB 181 FKDLTKVEVPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEEKAIALGV 240
 QY 241 AIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVEEA 300
 DB 241 AIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVEEA 300
 QY 301 TQSLYPLIGANGMDWMEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSQTSRL 360
 DB 301 TQSLYPLIGANGMDWMEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSQTSRL 360
 QY 361 DYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400
 DB 361 DYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400

RESULT 4
 ABR64305
 ID ABR64305 standard; protein; 400 AA.
 XX
 AC ABR64305;
 XX
 DT 16-SEP-2003 (first entry)
 XX
 DE Acetohydroxyacid isomeroreductase.
 XX
 KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
 XX
 OS Neurospora crassa.
 XX
 PN FR2829363-A1.
 XX
 PD 14-MAR-2003.
 XX
 PF 10-SEP-2001; 2001FR-00011689.

XX 10-SEP-2001; 2001FR-00011689.
 PR (AVET) AVENTIS CROPS SCIENCE SA.
 XX
 PA Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX
 PI WPI; 2003-405775/39.
 XX
 DR Treatment of crops, useful for controlling fungi on, e.g. cereals,
 XX potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroreductase.
 PT
 XX Claim 2; Fig 1; 66pp; French.
 PS
 XX The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (I) of acetohydroxyacid
 CC isomeroreductase. (I) are used for curative or preventative treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
 CC to illustrate the invention
 CC
 SQ Sequence 400 AA;

Query Match 88.6%; Score 1856; DB 6; Length 400;
 Best Local Similarity 86.8%; Pred. No. 9.6e-169;
 Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRAT--RKAAPVTOQOIRGVKTMDFEA 58
 DB 1 MAARNCTKALRPMARQLATPAVQRRTFVAASAVRASVAVKAAAPARQVGRVKTMDFA 60
 QY 59 GHKEQVWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSW 118
 DB 61 GHKEQVWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSW 120
 QY 119 KDAVQDQGWPGKMLFEVDIAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSHGFS 178
 DB 121 EDAIQDQGWPGKMLFEVDIAISRGTVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 180
 QY 179 PVFKDLTKVEVPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEEKAIAL 238
 DB 181 PVFKDLTKVEVPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEEKAIAL 240
 QY 239 GVAIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVE 298
 DB 241 GVAIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVE 300
 QY 299 EATQSLYPLIGANGMDWMEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSQTSR 358
 DB 301 EATQSLYPLIGANGMDWMEACSTTARRGAIDWTPFKDALKPVFNQLYDSVKNGDERKR 360
 QY 359 SLDYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400
 DB 361 SLEYNQSDPYREKYAEEMEEIRNLEIWRAGK--RSIRPENQK 400

RESULT 5
 ADV16810
 ID ADV16810 standard; protein; 403 AA.
 XX
 AC ADV16810;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE M graminicola ketol-acid reductoisomerase KAR1 seqid 9.
 XX substrate inhibition; antibiotic; gene disruption;
 KW ketol-acid reductoisomerase; KAR1; enzyme.
 XX
 OS Mycosphaerella graminicola.
 XX
 PN WO2004104176-A2.

XX 02-DEC-2004.
XX 17-MAY-2004; 2004WO-US015404.
XX 15-MAY-2003; 2003US-0470947P.
XX 19-MAY-2003; 2003US-0471615P.
XX 21-MAY-2003; 2003US-0472242P.
XX (PARA-) PARADIGM GENETICS INC.
XX Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC,
PI Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;
PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
XX WPI; 2005-021202/02.
DR N-PSDB; ADV16802, ADV16808, ADV16809.
XX
XX Identifying a test compound as a candidate for an antibiotic comprises
PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
PT with a test compound.
XX
XX Claim 50; SEQ ID NO 9; 179pp; English.
XX
XX The invention describes a method of identifying a test compound as a
CC candidate for an antibiotic comprising contacting ornithine
CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
CC or fungal pathogenicity-conferring gene with a test compound. The method
CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
CC ; and detecting the presence or absence of binding between the test
CC compound and the polypeptide or gene, where binding indicates that the
CC test compound is a candidate for an antibiotic. Also described are: an
CC isolated nucleic acid comprising a nucleotide sequence encoding a
CC polypeptide having at least 50% sequence identity to, or having at least
CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
CC polypeptide consisting essentially of the amino acid sequence of 400, 403
CC or 469 amino acids. The methods are useful for identifying inhibitors of
CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
CC pathogenicity-conferring gene as antibiotics. This is the amino acid
CC sequence of *Mycosphaerella graminicola* ketol-acid reductoisomerase KARI.
XX
SQ Sequence 403 AA;

Query Match 79.8%; Score 1671; DB 9; Length 403;
Best Local Similarity 78.4%; Pred. No. 5.4e-151;
Matches 315; Conservative 40; Mismatches 43; Indels 4; Gaps 1;

QY 1 MSARGFSKALRPMARQLATPAVORRSGFVAASSMVRAT---RKAAPVATQQQIRGVKTM 56
DB 1 MASNATRALRASLRQLKAPQVQORGFVAANRPSLVPQAQVTSFVQVGRGAKTV 60

QY 57 FAGHKQWVERADWPKEKLEYPKDDTLALIGYSGHGGGLNLDNGLNVIIVGRKDGK 116
DB 61 FAGDEKVFERDDWPKEKLEYPKDDTLALIGYSGHGGGLNLDNGLNVIIVGRKGG 120

QY 117 SKDANVDQGVKPNLFEVDEALSRGTVMNLLSDAAQSETWPAKQITKGTLYFSHG 176
DB 121 SWKEAEGDGVGVEKNLFDIDTAIGKTIIMNLLSDAAQSETWPHIKPMLTKGTLYFSHG 180

QY 177 FSPVFKDLTKVEVPTDDVILCAPKSGRTVRSFLFREGINSFSAVQDVGTGEAEKAI 236
DB 181 FSPVFKDQTKVEVPTDIDVILVAPKSGRTVRLFKEGINSIALFDQVTGKAEKAI 240

QY 237 ALGVAIGSGYLYKTTKEKVEYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNET 296
DB 241 ALGVAIGSGYLYKTTKEKVEYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNET 300

QY 297 VEATOSLYPLICANGMDMYEACSTTARRGADWSPRKDALKVPFNQLYDSVKDGET 356
DB 301 VEATOSLYPLIKNMGMDMYEACSTTARRGADWSPRKDALKVPFNQLYDSVKDGET 360

OY 357 QRSLDYNSQDYREKYAEEMBEIRNLEIWRAGKAVRSRLEN 398
DB 361 QRTMEYAGKDYREAFEXEMBEIRNLEIWRAGKAVRSRLEN 402

RESULT 6
ABJ26477
ID ABJ26477 standard; protein; 396 AA.
XX AC ABJ26477;
XX
XX 16-APR-2003 (first entry)
DT Aspergillus fumigatus essential gene protein #1135.
DE
XX Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection;
KW cancer; contamination; biofilm; antibody; immune response.
XX
XX *Aspergillus fumigatus*.
OS
XX WO200286090-A2.
PN
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013142.
PF
XX 23-APR-2001; 2001US-0285697P.
PR 27-APR-2001; 2001US-0287066P.
PR 05-JUN-2001; 2001US-0295890P.
PR 09-JUL-2001; 2001US-0303899P.
PR 31-AUG-2001; 2001US-0316362P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
PI WPI; 2003-093124/08.
DR
XX
XX New purified or isolated nucleic acids of essential genes of *Aspergillus*
PT *fumigatus*, useful for treating or preventing infections by *A. fumigatus*,
PT or for treating a non-infectious disease in a subject e.g. cancer.
XX
PS Disclosure; Page; 175pp; English.
XX
XX The invention relates to novel purified or isolated nucleic acids of
CC essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of
CC the invention are used to treat or prevent infections by a pathogenic
CC organism such as *A. fumigatus*, to treat a non-infectious disease in a
CC subject (e.g. cancer), to prevent or contain contamination of an object
CC by *A. fumigatus*, or to prevent or inhibit formation on a surface of a
CC biofilm comprising *A. fumigatus*. The polynucleotides are useful for
CC expressing recombinant protein for characterisation, screening or
CC therapeutic use, as markers for host tissues in which the pathogenic
CC organisms invade or reside, for comparing with the DNA sequence of *A.*
CC *fumigatus* to identify duplicated genes or paralogues having the same or
CC similar biochemical activity and/or function, for comparing with DNA
CC sequences of other related or distant pathogenic organisms to identify
CC potential orthologous essential or virulence genes, for selecting and
CC making oligomers for attachment to a nucleic acid array for examination
CC of expression patterns, for raising anti-protein antibodies, as an
CC antigen to raise anti-DNA antibodies or to elicit another immune
CC response, and for identifying polynucleotides encoding the other protein
CC with which binding occurs or to identify inhibitors of the binding
CC interaction. The polypeptides may be used to raise antibodies or to
CC elicit immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as a marker for
CC host tissues in which pathogenic organism invade or reside, and to
CC isolate correlative receptors or ligands in the case of virulence
CC factors. This sequence represents a protein of one of the essential genes
CC of *Aspergillus fumigatus* of the invention
XX
SQ Sequence 396 AA;

Query Match 79.7%; Score 1668; DB 6; Length 396;
 Best Local Similarity 79.1%; Pred. No. 1e-150;
 Matches 318; Conservative 42; Mismatches 34; Indels 8; Gaps 4;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRATKAA--VAPTOQOQIRGVKTMDFPA 58
 1 MASRGLPRALR-LAR-VAAP----RTVISALPRPALAKAATRVAASTAPRGVKTITAPA 54

QY 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGKSW 118
 55 DSKETVYERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGASW 114

QY 119 KDAVDGQWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKQITKGTLYFSHGFS 178
 115 KEAQDQWIPGKNLFDLTVAVQGTIVMNLSDAAQSETWPLKPLITKGTLYFSHGFS 174

QY 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSIFREGRGINSFVAYQDVTGEAEKAIAM 238
 175 PVFKELTKVDVDPKVDVILVAPKSGRTVRSIFREGRGINSFVAYQDVTGEAEKAIAM 234

QY 239 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 235 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 294

QY 299 EATQSLYPLIGANGMDWMYEAACSTTARRGAIDWSSRFKOTLKPIFNELYSVRDGTETKR 358
 295 EATQSLYPLIGANGMDWMYEAACSTTARRGAIDWSSRFKOTLKPIFNELYSVRDGTETKR 354

QY 359 SLDYNQSDPYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQK 400
 355 SLEYNQSDPYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQK 396

RESULT 7
 ABJ26502
 ID ABJ26502 standard; protein; 508 AA.

XX AC ABJ26502;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #1160.
 XX KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 XX KW cancer; contamination; biofilm; antibody; immune response.
 XX OS Aspergillus fumigatus.
 XX PN WO200286090-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013142.
 XX PR 23-APR-2001; 2001US-0285697P.
 XX PR 27-APR-2001; 2001US-0287066P.
 XX PR 05-JUN-2001; 2001US-0295890P.
 XX PR 09-JUL-2001; 2001US-0303899P.
 XX PR 31-AUG-2001; 2001US-0316362P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
 XX DR WPI; 2003-093124/08.
 XX PT New purified or isolated nucleic acids of essential genes of Aspergillus
 XX PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 XX PT or for treating a non-infectious disease in a subject e.g. cancer.
 XX PS Disclosure; Page; 175pp; English.
 XX CC The invention relates to novel purified or isolated nucleic acids of

essential genes of Aspergillus fumigatus. The isolated nucleic acids of
 the invention are used to treat or prevent infections by a pathogenic
 organism such as A. fumigatus, to treat a non-infectious disease in a
 subject (e.g. cancer), to prevent or contain contamination of an object
 by A. fumigatus, or to prevent or inhibit formation on a surface of a
 biofilm comprising A. fumigatus. The polynucleotides are useful for
 expressing recombinant protein for characterisation, screening or
 therapeutic use, as markers for host tissues in which the pathogenic
 organisms invade or reside, for comparing with the DNA sequence of A.
 fumigatus to identify duplicated genes or paralogues having the same or
 similar biochemical activity and/or function, for comparing with DNA
 sequences of other related or distant pathogenic organisms to identify
 potential orthologous essential or virulence genes, for selecting and
 making oligomers for attachment to a nucleic acid array for examination
 of expression patterns, for raising anti-protein antibodies, as an
 antigen to raise anti-DNA antibodies or to elicit another immune
 response, and for identifying polynucleotides encoding the other protein
 with which binding occurs or to identify inhibitors of the binding
 interaction. The polypeptides may be used to raise antibodies or to
 elicit immune response, as a reagent in assays designed to quantitatively
 determine levels of the protein in biological fluids, as a marker for
 host tissues in which pathogenic organism invade or reside, and to
 isolate correlative receptors or ligands in the case of virulence
 factors. This sequence represents a protein of one of the essential genes
 of Aspergillus fumigatus of the invention

Sequence 508 AA;

Query Match 79.7%; Score 1668; DB 6; Length 508;
 Best Local Similarity 79.1%; Pred. No. 1.5e-150;
 Matches 318; Conservative 42; Mismatches 34; Indels 8; Gaps 4;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRATKAA--VAPTOQOQIRGVKTMDFPA 58
 113 MASRGLPRALR-LAR-VAAP----RTVISALPRPALAKAATRVAASTAPRGVKTITAPA 166

QY 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGKSW 118
 167 DSKETVYERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGASW 226

QY 119 KDAVDGQWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKQITKGTLYFSHGFS 178
 227 KEAQDQWIPGKNLFDLTVAVQGTIVMNLSDAAQSETWPLKPLITKGTLYFSHGFS 286

QY 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSIFREGRGINSFVAYQDVTGEAEKAIAM 238
 287 PVFKELTKVDVDPKVDVILVAPKSGRTVRSIFREGRGINSFVAYQDVTGEAEKAIAM 346

QY 239 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 347 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 406

QY 299 EATQSLYPLIGANGMDWMYEAACSTTARRGAIDWSSRFKOTLKPIFNELYSVRDGTETKR 358
 407 EATQSLYPLIGANGMDWMYEAACSTTARRGAIDWSSRFKOTLKPIFNELYSVRDGTETKR 466

QY 359 SLDYNQSDPYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQK 400
 467 SLEYNQSDPYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQK 508

RESULT 8
 ABJ25902
 ID ABJ25902 standard; protein; 388 AA.

XX AC ABJ25902;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #560.
 XX KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 XX KW cancer; contamination; biofilm; antibody; immune response.

Db 241 GYVQTTTFRVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSL 300
 QY 305 YPLIGANGMDWYACSTTARRGAIOWSPRFKDALKPVFNQLYDSVKDGSSTORSLDYNS 364
 Db 301 YPLIGKGYMDWYACSTTARRGALDWYPIFNALKPVFQDLYESTKNGTETKRSLENS 360
 QY 365 QPDYREKYEAEMBEIRNLEIWRAGKAVRSIRPENQ 399
 Db 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395

RESULT 13
 ADK64188
 ID ADK64188 standard; protein; 395 AA.
 AC
 AC ADK64188;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 XX Disease treating protein complex-derived protein #1281.
 DE
 XX protein complex; drug target; diagnosis.
 KW
 XX Unidentified.
 OS
 XX
 FN EPI338608-A2.
 XX
 PD 27-AUG-2003.
 XX
 XX 20-DEC-2002; 2002EP-00102902.
 PF
 XX 20-DEC-2001; 2001EP-00130253.
 PR
 XX (CELL-) CELLZOME AG.
 PA
 XX
 PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK64189.
 XX

New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.

Disclosure; SEQ ID NO 2561; 13pp; English.

The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drug targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).

Sequence 395 AA;

Query Match 71.8%; Score 1503; DB 7; Length 395;
 Best Local Similarity 72.9%; Pred. No. 6.8e-135;

Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;
 QY 10 LRPMARQL--ATPAVQRSSFVAASSMVRATKAA--VAPTQQQIRGVKTMDFAGHKEQV 64
 Db 2 LRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKP-MITTRGLKQINFGTGVETV 60
 QY 65 WERADWPKEKLELYFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSKWDAVOD 124
 Db 61 YERADWPKEKLDYFKNDTFALIGYSGQGHGQGLNLDNGLNVIIGVRKDGASWKAATD 120
 QY 125 GWVPGKNLFEVDEAISRGTVIMNLLSDAAOSETWPAKLPQITKGTLYFSGHGRSPVPKDL 184
 Db 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAOSETWPAKLPQITKGTLYFSGHGRSPVPKDL 180
 QY 185 TKVEVPTDVIDILCAPKSGSGRTVRSFRPREGINSSPANTYQDVTGEAEKAIALGVAIGS 244
 Db 181 THVEPPKDLVILVAPKSGSGRTVRSFRPREGINSSPANTYQDVTGEAEKAIALGVAIGS 240
 QY 245 GYLYKTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNVEATQSL 304
 Db 241 GYVQTTTFRVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSL 300
 QY 305 YPLIGANGMDWYACSTTARRGAIOWSPRFKDALKPVFNQLYDSVKDGSSTORSLDYNS 364
 Db 301 YPLIGKGYMDWYACSTTARRGALDWYPIFNALKPVFQDLYESTKNGTETKRSLENS 360
 QY 365 QPDYREKYEAEMBEIRNLEIWRAGKAVRSIRPENQ 399
 Db 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395

RESULT 14
 ADB70124
 ID ADB70124 standard; protein; 409 AA.
 AC ADB70124;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE C. neoformans amino acid sequence SEQ ID NO:3168.
 XX
 KW fungicide; gene therapy; infection.
 XX
 OS Cryptococcus neoformans.
 XX
 FN WO2003052076-A2.
 PD 26-JUN-2003.
 XX
 PF 17-DEC-2002; 2002WO-US040225.
 XX
 PR 17-DEC-2001; 2001US-0341261P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Zamudio C, Eroshkin AM;
 XX
 DR WPI; 2003-533017/50.
 DR N-PSDB; ADB69041.
 XX
 PT New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
 PT
 XX
 PS Claim 9; SEQ ID NO 3168; 136pp; English.
 XX

The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.1579 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-1
Perfect score: 2094
Sequence: 1 MSARGFSKALRPMPARQLATP.....SIWRAGKAVRSLRPENQKQK 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	88.6	400	1 JCI1428	ketol-acid reducto
2	1503	71.8	395	1 A24709	ketol-acid reducto
3	1499.5	71.6	404	2 T40532	ketol-acid reducto
4	490	23.4	342	2 C69644	ketol-acid reducto
5	481.5	23.0	333	2 F70407	acetoxyhydroxy acid
6	479	22.9	331	2 AC1694	ketol-acid reducto
7	475	22.7	331	2 AB1323	ketol-acid reducto
8	473	22.6	332	2 H75044	ketol-acid reducto
9	472	22.5	337	2 A96911	ketol-acid reducto
10	462.5	22.1	336	2 G95051	ketol-acid reducto
11	462.5	22.1	340	2 C84032	ketol-acid reducto
12	462.5	22.1	340	2 C97922	ketol-acid reducto
13	461	22.0	336	2 D72362	ketol-acid reducto
14	455	21.7	348	1 F64492	ketol-acid reducto
15	453.5	21.7	335	2 C90204	ketol-acid reducto
16	449	21.4	367	1 A47037	ketol-acid reducto
17	447	21.3	581	2 T06825	ketol-acid reducto
18	446	21.3	340	2 B86778	ketol-acid reducto
19	441	21.1	591	1 S30145	ketol-acid reducto
20	441	21.1	591	2 T45681	ketol-acid reducto
21	436	20.8	331	2 AD2095	ketol-acid reducto
22	435	20.8	334	2 F89997	alpha-keto-beta-hy
23	428	20.4	344	1 S35440	probable ketol-ac
24	427	20.4	363	2 C75387	ketol-acid reducto
25	427	20.4	595	1 S17180	ketol-acid reducto
26	424	20.2	337	2 C81801	ketol-acid reducto
27	424	20.2	337	2 F81066	ketol-acid reducto
28	409.5	19.6	332	2 H69497	ketol-acid reducto
29	406	19.4	333	2 A69059	ketol-acid reducto

ketol-acid reducto 30 401 19.1 340 2 G81411
ketol-acid reducto 31 401 19.1 366 2 E82634
acetolactate synth 32 391 18.7 332 2 T35830
ketol-acid reducto 33 388 18.5 338 1 C48648
ketol-acid reducto 34 387 18.5 338 2 E83059
ketol-acid reducto 35 361 17.2 333 1 JC5166
ketol-acid reducto 36 359 17.1 343 2 T45415
probable ilvC prot 37 356.5 17.0 333 2 D70855
ketol-acid reducto 38 355 17.0 333 2 H87120
ketol-acid reducto 39 349.5 16.7 339 2 AB2824
ketol-acid reducto 40 349.5 16.7 339 2 D97602
hypothetical prote 41 345.5 16.5 339 2 G87511
ketol-acid reducto 42 333.5 15.9 339 2 AB3330
ketol-acid reducto 43 327 15.6 330 1 B64561
ketol-acid reducto 44 318 15.2 330 2 A71945
ketol-acid reducto 45 306.5 14.6 491 1 ISECKR

ALIGNMENTS

RESULT 1

JCI1428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N;Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
C;Species: Neurospora crassa
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JCI1428
R;Sista. H.; Bowman, B.
Gene 120, 115-118, 1992
A;Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-b-
A;Reference number: JCI1428; MUID:93013010; PMID:1398116
A;Accession: JCI1428
A;Molecule type: DNA
A;Residues: 1-400 <STS>
A;Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:g168821; PTDN:
C;Genetics:
A;Gene: ilv-2
A;Map position: V
A;Introns: 68/1; 78/3; 170/3; 392/3
C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F;87-273/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 88.6%; Score 1856; DB 1; Length 400;
Best Local Similarity 86.8%; Pred. No. 5-2e-134;
Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MSARGFSKALRPMPARQLATPAVQRRSFVAASSMVRAT--RKAAPVPTQQQIRGVKTTMDFA 58
Db 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVAAAPARQQVRGVKTTMDFA 60
Qy 59 GHKEOWERADWPEKLELVFKDDTLALTYGSGQGHGQGLNLRDGLNLIIVGRKQKSW 118
Db 61 GHKEVHERADWPEKLLDYFKNDTLALTYGSGQGHGQGLNLRDGLNLIIVGRKQKSW 120
Qy 119 KDAVQDQWPGKNLFEVDRAISRTVIMNLLSDAAOSETWPAKLPQITTKGKTLFYSHGFS 178
Db 121 EDIAQDQWPGKNLFDVDEAISRTVIMNLLSDAAOSETWPHIKPQITTKGKTLFYSHGFS 180
Qy 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSLSFREGGINSSPAVYQDVTGEAEKAIAL 238
Db 181 PVFKDLTKVEPTDVIDVILVAPKSGRTVRSLSFREGGINSSPAVYQDVTGKAKEKAVAL 240
Qy 239 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGHGFLAQYEVLRERGHSPSEAFNIVE 298
Db 241 GVAIGSGYLYETTFEKEVYSDLYGERGCLMGGHGFLAQYEVLRERGHSPSEAFNIVE 300
Qy 299 EATQSLYPLIGANGMDWMYEAECTTARRGAIDWSPRFKDALKPVFNOLYDVSVDGSGSTOR 358
Db 301 EATQSLYPLIGANGMDWMFDACSTTARRGAIDWTPFKDALKPVFNNLHYDVSVDGDERKR 360
Qy 359 SLDYNQDPYREKYEAEMEIRNLEIWRACKAVRSLRPENQK 400

keto-acid reductoisomerase ilvC - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: C69644
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69644
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <KUN>
A:Cross-references: UNIPROT:P37253; UNIPARC:UPI00000380EE; GB:Z99118; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductois
F:21-202/Domain: keto-acid reductoisomerase homology <KAR>
Query Match 23.4%; Score 490; DB 2; Length 342;
Best Local Similarity 36.7%; Pred. No. 8.6e-30;
Matches 122; Conservative 68; Mismatches 118; Indels 24; Gaps 11;
Qy 72 KEKLEVPKDTLALIGVSGHGGQGLNRLDNGLNVLIVGRKDGKSWKDAVQDGVPGKN 131
Db 11 KENVL---AKTVAVIGVSGHGHALNRLKESGVVDVIVGRQ-GKSFQAGD---GHK 62
Qy 132 LFEVDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLFSGHSPFVKDLTKVEVP 190
Db 63 VFSVKEAAQAELIIVLLPDEQQKVEAEIKBELTAGKSLVFAHGFNVHFQIVP---P 119
Qy 191 TDVDVILCAPKSGSRTVRSIFREGRGINSFPAVQDVTGAEKAIAGVAIG---SGYL 247
Db 120 ADVDDVFLVAPKPGHLVRRTYEQGAGVPALFAIQDVTGGEARDKALAYAKGIGGARAGVL 179
Qy 248 YKTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNVEATQSLYPL 307
Db 180 -ETTFKEETDLDLFGQVLCGLSALVKAGFETLTAGYQPELAYVECLHE-LKLIVDL 237
Qy 308 IGANGMDMYEACSTTARRGAIDMSPRFKDA-LKPVFNQLYDSKDGSETQRSIDYN--S 364
Db 238 MYEGLAGMYSISDTAQWGDVFSVPRVVDKVKESMKVLDIQNGTFAKEVIVENQVN 297
Qy 365 QPDYREKYEAEIRNLEIWRAGKAVRSRSP 396
Db 298 RPRFNAINASENEH---QIEVVGRKLRNMP 325
RESULT 5
F70407
acetohydroxy acid isomeroreductase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C:Accession: F70407
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98156666; PMID:9537320
A:Accession: F70407
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-333 <AQF>
A:Cross-references: UNIPROT:O67289; UNIPARC:UPI0000056582; GB:AE000730; NID:G2983674; P1
A:Experimental source: strain VF5
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductois
F:21-203/Domain: keto-acid reductoisomerase homology <KAR>
Query Match 23.0%; Score 481.5; DB 2; Length 333;
Best Local Similarity 33.3%; Pred. No. 3.7e-29;
Matches 110; Conservative 72; Mismatches 135; Indels 13; Gaps 6;
Qy 70 WPKEKLEVPKDTLALIGVSGHGGQGLNRLDNGLNVLIVGRKDGKSWKDAVQDGVPG 129
Db 6 YDEADSIDLKDVIALIGVSGHGHALNRLDNGLNVLIVGRKDGKSWKDAVQDGVPG 62
Qy 130 KNLFEVDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLFSGHSPFVKDLTKVE 188
Db 63 -EYVTPREAAKRAADIIMFLIPDTPVQEVYKNEVEPELNSKTLAFAGFNIHFQIVP-- 119
Qy 189 VPTDNDVILCAPKSGSRTVRSIFREGRGINSFPAVQDVTGAEKAIAGVAIGS--GY 246
Db 120 -PKDQVDFWVAPKPGHLVRRWYTEGKVPALVAIHQDASGTCCKALAYAKGIGATRA 178
Qy 247 LYKTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNVEATQSLYPL 306
Db 179 VIETTFKEETDLDLFGQVLCGLSALVKAGFETLTAGYQPELAYVECLHE-LKLI 237
Qy 307 IGANGMDMYEACSTTARRGAIDMSPRFKDA-LKPVFNQLYDSKDGSETQRSIDYN 366
Db 238 LIYEHGISMGRYSISDTAKYGVDTGRGRIYKVKVPYMEKTLLEIQGFEFAREWILEN 297
Qy 367 DYREKYEAEIRNLEIWRAGKAVRSRSP 396
Db 298 --RPVYVALLERDRHLVKEVGEELRKNMP 325
RESULT 6
AC1694
keto-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AC1694
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maicournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maicournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1694
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <GLA>
A:Cross-references: UNIPARC:UPI00000CC759; GB:AL592022; PIDN:CAC97323.1; PID:G16414607;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductoisom
Query Match 22.9%; Score 479; DB 2; Length 331;
Best Local Similarity 36.1%; Pred. No. 5.7e-29;
Matches 120; Conservative 59; Mismatches 129; Indels 24; Gaps 10;
Qy 78 YPKD-----DTLALIGVSGHGGQGLNRLDNGLNVLIVGRKDGKSWKDAVQDGV 128
Db 5 YVEDAVKNNALEGKTVAVIGVSGHGHALNRLDNGLNVLIVGRKDGKSWKDAVQDGV 61
Qy 129 GKNLFEVDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLFSGHSPFVKDLTKV 187
Db 62 --DVYSVSEAEKADVIMILLPDETQGETYENEIKPNLKNAGNALVFAHGFNIHF---DVI 116

QY	188	EVPTDQVILCAPKSGSRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIGS--G	245
Db	117	NPSPDQVFLVAPKPGHLVRRFTVEGAVPSLFAIQDQATGNARTALSAYAKIGATRA	176
QY	246	YLKTTTFKEVYSDLYGERGCLMGHMFVLAQYEVLRERGHSPSAFNETVEEATQSLY	305
Db	177	GVTIETTFKEETEDLDFGEQAVLCGGATHLIQAGFETLVEAGYQPELAYFEVLHE-MKLI	235
QY	306	PLIGANGMDWMYACSTTARRGAIDWSPRFKDA-LKPVFNQLYDYSVKDGETORSRLD	364
Db	236	DLMYEGMEKORHSIENTAEYGDYVSGPRVVTADTKKAMKEVLTDIQNGNFAKSFIND	295
QY	365	QPDYREKYAEEMEIRNLEINLRWAGKAVRSILRP	396
Db	296	N-GFKEFHRMKEQ-QGHQIEKVGAEIREMMP	325
RESULT 7			
AB1323			
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]			
C:Species: Listeria monocytogenes			
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004			
C:Accession: AB1323			
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker			
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.			
D.; Jones, L.M.; Karst, U.			
Science 294, 849-852, 2001			
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma			
ok, C.; Schluter, T.; Simoes, N.; Tlierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,			
A:Title: Comparative genomics of Listeria species.			
A:Reference number: AB1077; MUID:21537279; PMID:11679669			
A:Accession: AB1323			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-331 <GLA>			
A:Cross-references: UNIPARC:UPI0000054FF8; GB:NC_003210; PIDN:CAD00064.1; PID:gi6411439;			
A:Experimental source: strain EGD-e			
C:Genetics:			
A:Gene: ilvC			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois			
Query Match 22.7%; Score 475; DB 2; Length 331;			
Best Local Similarity 35.8%; Pred. No. 1.1e-28;			
Matches 119; Conservative 61; Mismatches 128; Indels 24; Gaps 10;			
QY	78	YFKD-----DTALICYGSGHGGQGLNLRDNGLVNIIGVRKDGKSWKDAVQDGWVP	128
Db	5	YBEDAVKNNALGKTVAVIGYSGQGHASHQNLNRDNGNNVIGIR-EGKSAESARNDGF--	61
QY	129	GKNLFEVDEAISRGTVIMNLLSDAAQSETPW-ALKPQITKGTLYFSHGSPSPVKDLTKV	187
Db	62	--DVISVSEADKADVIMILLPDTQGETYENIKENLKNAGSLVFAHGFNIHF---DVI	116
QY	188	EVPTDQVILCAPKSGSRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIGS--G	245
Db	117	NPSPDQVFLVAPKPGHLVRRFTVEGAVPSLFAIQDQATGNARTALSAYAKIGATRA	176
QY	246	YLKTTTFKEVYSDLYGERGCLMGHMFVLAQYEVLRERGHSPSAFNETVEEATQSLY	305
Db	177	GVTIETTFKEETEDLDFGEQAVLCGGATHLIQAGFETLVEAGYQPELAYFEVLHE-MKLI	235
QY	306	PLIGANGMDWMYACSTTARRGAIDWSPRFKDA-LKPVFNQLYDYSVKDGETORSRLD	364
Db	236	DLMYEGMEKORHSIENTAEYGDYVSGPRVVTADTKKAMKEVLTDIQNGNFAKSFIND	295
QY	365	QPDYREKYAEEMEIRNLEINLRWAGKAVRSILRP	396
Db	296	N-GFKEFHRMKEQ-QGHQIEKVGAEIREMMP	325
RESULT 8			
H75044			

ketol-acid reductoisomerase (ilvC) PAB0889 - Pyrococcus abyssi (strain Orsay)			
C:Species: Pyrococcus abyssi			
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004			
C:Accession: H75044			
R:anonymous, Genoscope			
submitted to the EMBL Data Library, July 1999			
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru			
A:Reference number: A75001			
A:Accession: H75044			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-332 <KAW>			
A:Cross-references: UNIPROT:O9UZ09; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID:			
A:Experimental source: strain Orsay			
C:Genetics:			
A:Gene: ilvC; PAB0889			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois			
F;24-206/Domain: ketol-acid reductoisomerase homology <KAR>			
Query Match 22.6%; Score 473; DB 2; Length 332;			
Best Local Similarity 35.4%; Pred. No. 1.6e-28;			
Matches 116; Conservative 71; Mismatches 123; Indels 18; Gaps 9;			
QY	73	EKLLBYFKDDTLALICYGSGHGGQGLNLRDNGLVNIIGVRKDGKSWKDAVQDGWVGKXL	132
Db	12	EVSMDILDKTKTVAVIGYGNQGEAQAKNMDSGVHVILGLRPSGSSWKRAEKDGF---EV	67
QY	133	FEVDEAISRGTVIMNLLSDAAQSETPW-PALKPQITKGTLYFSHGSPSPVKDLTKVEVPT	191
Db	68	YTIEEAVKRAIDVHILIPDLVQPKVYREHIEPYLREGQALGFSGHGFNIHYKQIVP---PE	124
QY	192	DVDVILCAPKSGSRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIG---SGYLY	248
Db	125	YDVIWVAPKSPGKRVREKILEGFGVPALVAVIYQDTGNAKOLALAWAKAIGCTRAGVI-	183
QY	249	KTTFEKVVSDLYBERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI	308
Db	184	ETTFKDESDLIIGQLVLVGGELIELIKKGFEVLVELGYPPPELAYFEACNEA-KLIMDLI	242
QY	309	GANGMDWYEACSTTARRGAIDWSPR-FKDALKVPFNQLYDYSVKDGETORSRLDYSQPD	367
Db	243	YERGFTGMLKAVSDTAKYGLTVGPKVIDDHVKENMKKFAERVRSQ---EFAKEWISKAD	299
QY	368	-VREKYAEEMEIRNLEINLRWAGKAVRSIL	394
Db	300	KASEVLEELMKPIEHEIEKVGKRFIRKM	327
RESULT 9			
A96911			
ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum			
C:Species: Clostridium acetobutylicum			
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004			
C:Accession: A96911			
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,			
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.			
J. Bacteriol. 193, 4823-4838, 2001			
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo			
A:Reference number: A96900; MUID:21359325; PMID:21359325			
A:Accession: A96911			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-337 <KUR>			
A:Cross-references: UNIPROT:Q97MV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1;			
A:Experimental source: Clostridium acetobutylicum ATCC824			
C:Genetics:			
A:Gene: CAC0091			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois			
Query Match 22.5%; Score 472; DB 2; Length 337;			
Best Local Similarity 34.2%; Pred. No. 2e-28;			
Matches 115; Conservative 65; Mismatches 132; Indels 24; Gaps 9;			

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Qy 76 LEYFKDDTLALIGYSGHGGIINLRDNLNLIIVGVRKDGSKWDKAVODGVHPGKNLFEV 135
Db 14 LNYLKKKIALIGSGGHAHALKESGLNVLVGLYDGSKSWKVAEDYGF----EYVEF 69

Qy 136 DEALSRGTVINMLLSDAASQETWPA-LKPQITKGTLYFSHGSPFVKDLTKVEVPTDVD 194
Db 70 ADVAKQAVVMILLPDEKQIYEASIKONLDEGDAJFFANGFNIHYNQIVP----PKNVD 126

Qy 195 VILCAPKSGRTVSLFRGGRGINSFVAVQDVTGEAEKAIAGVAIG--SGYLYKTTTF 252
Db 127 VLMIAPIKPGHIVRRQYTGEGGVCLYAVHODYTGKKEIALAYGKGIGGTGGWMTTF 186

Qy 253 EKEVYSDLYGRCGLMGHGMFLAQYEVILBERGHSPEAFNEVEATQSLYPLICANG 312
Db 187 KIETETDLFGQAVLCGICCALINAGYDITREAGYSAENAYFECHF--MKMIVDLMYEGG 245

Qy 313 MDMMYEACSTTARRGAIDWSPR-FKDALKPVFNLQYDSVKDGSQTSRSL--DYNQPDYR 369
Db 246 MAKWYSISDTAEYGDYVVGNNRLINDNVRAEMKVKLTETIQGTFAKWILLENQTRGPAFN 305

Qy 370 EKYAEAEIRNLEIWRAGKAVRSL-----RPNQ 399
Db 306 ARRIEADR----EIEKVGKRLGMGWINENPSNE 337

RESULT 10
G95051
ketol-acid reductoisomerase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C:Accession: G95051
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid-
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickley, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95051
A:Molecule type: DNA
A:Residues: 1-336 <KUR>
A:Cross-references: UNIPROT:Q97SD7; UNIPARC:UPI000000C9C91; GB:AE005672; PIDN:AAK74608.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0447
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom-
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Query Match 22.1%; Score 462.5; DB 2; Length 336;
Best Local Similarity 36.3%; Pred. No. 1.1e-27;
Matches 122; Conservative 54; Mismatches 131; Indels 29; Gaps 10;

Qy 76 LEYFKD-----DTLALIGYSGHGGIINLRDNLNLIIVGVRKDGSKWDKAVODGVW 127
Db 1 MEYKVKVVAALDGKKTAVIGYSGGHAHAQNLRDSDGRVLIIGVR-PGKSFDRKXEDGF- 58

Qy 128 PGKNLFEVDAISRGTVINMLLSDAASQETWPA-LKPQITKGTLYFSHGSPFVKDLTK 186
Db 59 ---DTVTVAETKLADVIMILADEIQEILYEAIAPNLEAGNAVGFANGFNTHFE---F 112

Qy 187 VEVPTDVIDLCPKSGRTVSLFRGGRGINSFVAVQDVTGEAEKAI--ALGVAIGS 244
Db 113 IKVPADVDFMPCAPKPGHILVRRTYERGFVPAALYVQDQATGNNAKNIAMDCWGVGAAR 172

Qy 245 GYLYKTTTFEYVSDLYGRCGLMGHGMFLAQYEVILBERGHSPEAFNEVEATQSL 304
Db 173 VGLLETTYKEETEDLFGQAVLCGGLTALIRAGFEVLTEAGYAPLAYEVLHE--MKLI 231

Qy 305 YPLIGANGMDMYEACSTTARRGAIDWSPR-FKDALKPVFNLQYDSVKDGSQTSRSLDYN 363
Db 232 VDLIYEGFPKMQKQSISNTAEYGDYVVGNNRLINDNVRAEMKVKLTETIQGTFAKWILLENQTRGPAFN 305

Qy 364 SQPDY---REKYAEAEIRNLEIWRAGKAVRSLRP 396
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Db 290 ---DYKAGRPKLTAAYREQAANLEIEKVGAELRKAMP 322

RESULT 11
C84032
ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession: C84032
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira-
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84032
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <STO>
A:Cross-references: UNIPROT:Q9K8E7; UNIPARC:UPI000012D53B; GB:AP001517; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom-
er

Query Match 22.1%; Score 462.5; DB 2; Length 340;
Best Local Similarity 35.4%; Pred. No. 1.1e-27;
Matches 115; Conservative 57; Mismatches 124; Indels 29; Gaps 9;

Qy 83 TIALIGYSGHGGIINLRDNLNLIIVGVRKDGSKWDKAVODGVHPGKNLFEVDAISRG 142
Db 19 TVAILIGYSGGHAHAQNLRDSDGRVLIIGVR-PGKSWDKAAEDGF---QYYSVREAAASRA 73

Qy 143 TVIMNLLSDAAQSETWPA-LKPQITKGTLYFSHGSPFVKDLTKVEVPTDVIDVILCAPK 201
Db 74 DVIMILLPDEHQPTVYKNEIEPELSGKTLAFAGFNVHFNQIVP---PATVDVFLAPK 130

Qy 202 GSGRTVSLFRGGRGINSFVAVQDVTGEAEKAIAGVAIGSY--LYKTFEKEVYSD 259
Db 131 GPGLVRRTYVDCGAVGVLVAVYQDQATGQAKIALAYSKMNGSARAGVITTTFOEETED 190

Qy 260 LYGERCLMGHGMFLAQYEVILBERGHSPEAFNEVEATQSLYPLICANGMDMYEAC 319
Db 191 LFGEQAVLCGTSALVKGAFETLVEAGYQPEVAFYFCLHE-LKLIIVDMYEGGLEYNRY 249

Qy 320 CSTTARRGAIDWSPRFKDA-LKEVFNQLYDSVKDGS-----ETQKSLDYNQPDYREK 371
Db 250 ISDTAQWGFQAGPRVVTATKQAMKDIILSDITQTKFAKWILENQAN-----RPE 300

Qy 372 YEAEAEIRNLEIWRAGKAVRSLRP 396
Db 301 FTAINERKKNHPLVVGVRELREMP 325

RESULT 12
C97922
ketol-acid reductoisomerase (EC 1.1.1.86) [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 05-Oct-2004
C:Accession: C97922
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E-
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M-
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C97922
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <KUR>
A:Cross-references: UNIPROT:Q8DR03; UNIPARC:UPI000005143B; GB:AE007317; PIDN:AAK99207.1;
C:Genetics:
A:Gene: ilvC
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C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase; isomerase; oxidoreductase	
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Matches 122; Conservative 54; Mismatches 131; Indels 29; Gaps 10;	
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DB	5 MEYKDVKVAALDGKKIAGVIGYSGHQAHAQNLRDSDGRDVIIGVR-PGKSFDFKAKEDGF- 62
QY	128 PGKNLFEVDIAISRGTVIMNLLSDAAQSETWPA-LKPQITKGTLYFSHGSPSPVFKDLTK 186
DB	63 ---DITVTAETLADVIMILAPDEIQELYEAEIAPNLNAGNAVGAHGFNIHFE---F 116
QY	187 VEYPTDVTILCAPKSGRTRVSLRFRGGINSSFAVYQDVTGEAEKAI--ALGVAIGS 244
DB	117 IKVPADVDFMCAKPGHVLRTYEEGFGVPALYAVYQDATGNANKNIAMWCCKVGGAAR 176
QY	245 GYLTKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 304
DB	177 VGLLETTYKEETEDLFGQAVLCGGLTALIEAGFEVLTEAGYAPELAYFEVLHE-WKLI 235
QY	305 YPLIGANGMDWMEACSTTARRGAIDWSPR-FKDALKPVFNQLYDSVKGSGSETQSRSLDYN 363
DB	236 VDLIYEGGFKMKRQSIINTAEYGDYVSGPRVITEQVKENMKAVLADIQNGKPFANDFN-- 293
QY	364 SQPDY---REKYAEEMEEIRNLRIWRAGKAVRSLRP 396
DB	294 ---DYKAGRPKLTAYREQAANLEIKVGAEIRKAMP 326
RESULT 13	
D72362	
ketol-acid reductoisomerase - Thermotoga maritima (strain MSB8)	
C;Species: Thermotoga maritima	
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004	
C;Accession: D72362	
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.	
Nature 399, 323-329, 1999	
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq	
A;Reference number: A72200; PMID:99287316; PMID:10360571	
A;Accession: D72362	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-336 <ARN>	
A;Cross-references: UNIPROT:Q9WZ20; UNIPARC:UPI000012D560; GB:AE001730; GB:AB000512; NID	
A;Experimental source: strain MSB8	
C;Genetics:	
A;Gene: TW0550	
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase	
F;21-203/Domain: ketol-acid reductoisomerase homology <NAR>	
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DB	6 YDKDADNLNLIKOKKIAIIGYSGHQAHAQNLKDSGLNVVGLREGSKSKWKAEEQ---G 61
QY	130 KNLFVEDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGTLYFSHGSPSPVFKDLTKVE 188
DB	62 LVTKTIEAAKEADIIMILPDEHQPEIYKYEKHTGKMLMPAHGFNIHYHQIIP-- 119
QY	189 VPTDVTILCAPKSGRTRVSLRFRGGINSSFAVYQDVTGEAEKAIAL--GVAIGSGY 246
DB	120 -PKNVDTMTAPKSPGHVIRREYVEGREGVPALVAVYQDTYGRAKDIALAYAKGIGVTRAG 178
QY	247 LYKTTTEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSLYP 306

DB	179 VIETTFPEETEDLFGQAVLCGGVTALIKAGFETLVDAGYQVEIAYFECLNE-LKLIVD 237
QY	307 LIGANGMDWMEACSTTARRGAIDWSPR-FKDALKPVFNQLYDSVKGSGSETQSRSLDY--NS 364
DB	238 LIYEGGLSPMRYSVSNATBYG--DYISQBKIYTVKEVRENMKQMLKDIOGTQKFAKWILDEN 295
QY	365 QPDYREKYAEEMEEIRNLRIWRAGKAVRSLRP 396
DB	296 QAGRPYFYTWKKESEHL-IEKVGKELRKOMP 326
RESULT 14	
F64492	
ketol-acid reductoisomerase (EC 1.1.1.86) - Methanococcus jannaschii	
C;Species: Methanococcus jannaschii	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004	
C;Accession: F64492	
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	
Science 273, 1058-1073, 1996	
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.	
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.	
A;Reference number: A64300; PMID:96337999; PMID:8688087	
A;Accession: F64492	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-348 <BUL>	
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C;Genetics:	
A;Map position: FOR1521365-1522411	
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase	
C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase	
F;39-221/Domain: ketol-acid reductoisomerase homology <NAR>	
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Best Local Similarity	33.3%; Pred. No. 4.1e-27;
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DB	24 YDKYDTFADVKDKDTIAGVYGSQRAQNALNMKDSGLNVIGLVRPNGASNKAIKD---G 79
QY	130 KNLFVEDEAISRGTVIMNLLSDAAQSETW-PALKPQITKGTLYFSHGSPSPVFKDLTKVE 188
DB	80 HKVMTIEAAEKADIIMILPDEVOPAVYKKEIYELTEGKTIISFSGNIHY---GFTR 136
QY	189 VPTDVTILCAPKSGRTRVSLRFRGGINSSFAVYQDVTGEAEKAIALGVAIGSGY-- 246
DB	137 PPEVNIITMVAAPKSPGAMVRKTYEEGFGVPLVAVERYDTGDALQ--IALGMAKGIGLTRK 194
QY	247 --LYKTTTEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 304
DB	195 VGVIOQTTFREETEDLFGQAVLCGGVTALIKAAFELTLEAGYAPEMAYFETCHE-LKLI 253
QY	305 YPLIGANGMDWMEACSTTARRGAIDWSPR-FKDALKPVFNQLYDSVKGSGSETQSR- 362
DB	254 VDLIYQKGLQGWENVSNTAEYGGITRRARVINERSRKMKELIKEIQDRPAKWSLE- 312
QY	363 NSQPDYREKYAEEMEEIRNLE---IWRAGKAVRSL 394
DB	313 -----REAGFPFNLNRLREKHEHLIEKVGKELRKX 342
RESULT 15	
C92024	
ketol-acid reductoisomerase (ilvc-1) [imported] - Sulfolobus solfataricus	
C;Species: Sulfolobus solfataricus	
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004	
C;Accession: C92024	
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y	
Jong, I.; Jeffries, A.C.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.	
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.	

Search completed: March 22, 2006, 15:34:32
Job time : 22.1579 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 125.94 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248A-1

Perfect score: 2094

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2081	99.4	400	Q52F28_MAGGR	Q52f28 magnaportha
2	1881	89.8	402	ILV5_NEUCR	P38674 neurospora
3	1861.5	88.9	405	Q4HY40_GIBZE	Q4hy40 gibberella
4	1675	80.0	508	Q4WY4 ASPFU	Q4wy4 aspergillus
5	1673	79.9	400	Q5BA44_EMENI	Q5ba44 aspergillus
6	1581.5	75.5	398	Q5CAP8_YARLI	Q5caf8 yarrowia li
7	1542	73.6	399	Q5BL24_DEBHA	Q5bl24 debaryomyce
8	1530	73.1	397	Q6CY71_KIULA	Q6cy71 kluyveromyce
9	1526.5	72.9	400	Q59W5 CANAL	Q59w5 candida alb
10	1524.5	72.8	400	Q59X8 CANAL	Q59x8 candida alb
11	1505.5	71.9	399	Q6FXG6_CANGA	Q6fxg6 candida gla
12	1503	71.8	395	ILV5_YEAST	P06168 saccharomyc
13	1501	71.7	395	Q02341_YEAST	Q02341 saccharomyc
14	1499.5	71.6	404	ILV5_SCHFO	P78827 schizosacch
15	1489	71.1	395	Q02340_YEAST	Q02340 saccharomyc
16	1467.5	70.1	394	Q75CW4_ASHGO	Q75cw4 ashbya goss
17	1433.5	68.5	401	Q55048_CRYNE	Q55q48 cryptococcu
18	1433.5	68.5	401	Q5KFA0_CRYNE	Q5kfa0 cryptococcu
19	1416.5	67.6	401	Q96V25_CRYNE	Q96v25 cryptococcu
20	1253	59.8	625	Q4P572_USTWA	Q4p572 ustilago ma
21	1119	53.4	352	Q94135_9FUNG	Q94135 piromyces s
22	1102.5	52.7	362	Q5L9U3_BACFN	Q5l9u3 bacteroides
23	1102.5	52.6	359	Q8A612_BACFN	Q8a612 bacteroides
24	1100.5	52.6	347	Q64P11_BACFR	Q64p11 bacteroides
25	1043	49.8	344	Q847R5_ASTYP	Q847r5 aster yello
26	510.5	24.4	341	Q5KWJ2_GEOKA	Q5kwj2 geobacillus
27	507	24.2	341	Q8RL86_BACST	Q8rl86 bacillus st
28	494	23.6	332	1 ILV5_PVRFU	Q8u2a3 pyrococcus
29	490	23.4	342	1 ILV5_BACSU	P37233 bacillus su
30	481.5	23.0	333	1 ILV5_AQUAE	Q67289 aquifex aeo
31	479	22.9	331	1 ILV5_LISIN	Q92a29 listeria in

RESULT 1

ID	Q52F28_MAGGR	PRELIMINARY;	PRT;	400	AA.
AC	Q52F28;				
DT	13-SEP-2005	(Tremblrel. 31, Created)			
DT	13-SEP-2005	(Tremblrel. 31, Last sequence update)			
DT	13-SEP-2005	(Tremblrel. 31, Last annotation update)			
DE	Hypothetical protein.				
GN	ORFNames=MG01808.4;				
OS	Magnaporthe grisea 70-15.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Sordariomycetes incertae sedis; Magnaporthaceae; Magnaportha				
OX	NCBI_TaxID=242507;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=70-15;				
RA	Biren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,				
RA	Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,				
RA	Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,				
RA	Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavsky L.,				
RA	Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,				
RA	Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,				
RA	Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,				
RA	David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,				
RA	Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,				
RA	Erickson J., Farina L., Fero S., Ferreira P., Fischer H.,				
RA	Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,				
RA	Gairke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,				
RA	Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,				
RA	Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,				
RA	Jaffe D., Jones C., Kamal M., Kamat A., Kamvysellis M., Karlsson E.,				
RA	Kells C., Kieu A., Kianer P., Kodira C., Kulbokas E., Labutti K.,				
RA	Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,				
RA	Lindblad-ton K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,				
RA	Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,				
RA	Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,				
RA	McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,				
RA	Mesirov J., Mihalav A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,				
RA	Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,				
RA	Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,				
RA	Norbu N., O'donnell P., O'leary S., O'moto B., O'moto B.,				
RA	O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,				
RA	Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,				
RA	Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,				
RA	Rutman M., Schupbach R., Seaman C., Settillalli S., Sharpe T.,				
RA	Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,				
RA	Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,				
RA	Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,				
RA	Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Tophang K.,				
RA	Towey S., Teamlia T., Tsomo N., Vallee D., Vassiliev H.,				
RA	Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,				
RA	Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,				
RA	Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,				
RA	Zimmer A., Zody M., Lander E.;				

ALIGNMENTS

32	479	22.9	331	1	ILV5_LISNF	Q7ly36 listeria mo
33	476.5	22.8	336	1	ILV5_BACCL	Q73ba1 bacillus ce
34	476.5	22.8	336	2	Q6HLF4_BACHK	Q6hlf4 bacillus th
35	476.5	22.8	336	2	Q63DX9_BACCC	Q63dx9 bacillus ce
36	475	22.7	328	1	ILV5_PYRAE	Q8zte1 pyrobaculum
37	475	22.7	331	1	ILV5_LISMO	Q8y580 listeria mo
38	473.5	22.6	338	1	ILV5_BACCR	Q8y580 listeria mo
39	473	22.6	332	1	ILV5_CLOAB	Q9uz09 pyrococcus
40	472	22.5	337	1	ILV5_CLOAB	Q9uz09 pyrococcus
41	472	22.5	341	2	Q5WEN2_BACSK	Q5wmv0 clostridium
42	472	22.5	342	2	Q65GI7_BACLD	Q65gi7 bacillus li
43	469.5	22.4	336	1	ILV5_BACAN	Q65gi7 bacillus li
44	464.5	22.2	340	2	Q5LXV0_STR11	Q8lt69 bacillus an
45	464.5	22.2	340	2	Q5M2F2_STRT2	Q5lxx0 streptococc
						Q5m2f2 streptococc


```

RT  "The genome sequence of Magnaporthe grisea.";
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=70-15;
RA  Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=70-15;
RA  Zhu H., Blackmon B.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL: AACU01000121; EAA56157.1; -; Genomic_DNA.
DR  InterPro; IPR000506; ACh_isomrdctse.
DR  Pfam; PF01450; Transketo_C-like.
DR  TIGRFAMs; TIGR00465; ilvC; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 400 AA; 44723 MW; 4C89B9E1495B6D75 CRC64;

Query Match 99.4%; Score 2081; DB 2; Length 400;
Best Local Similarity 99.8%; Pred. No. 6e-141;
Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 MSARGFSKALRPWALQATPAVORRSPFAASSWVRATRKAAVAPTQOQIRGVKTMDFAGH 60
DB  1 MSARGFSKALRPWALQATPAVORRSPFAASSWVRATRKAAVAPTQOQIRGVKTMDFAGH 60
QY  61 KEQWERADWPKEKLLFEYFKDDTLALIGYSGHQGGLNRDNLNLIIGVRKDGSKWD 120
DB  61 KEQWERADWPKEKLLFEYFKDDTLALIGYSGHQGGLNRDNLNLIIGVRKDGSKWD 120
QY  121 AVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPAKPOITKGTLYPSHGFSVP 180
DB  121 AVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPAKPOITKGTLYPSHGFSVP 180
QY  181 FKDLTKVEVPTDNDVILCAPKSGRTVRSIFRGRGINSSFAVYQDVVTGAEKALALGV 240
DB  181 FKDLTKVEVPTDNDVILCAPKSGRTVRSIFRGRGINSSFAVYQDVVTGAEKALALGV 240
QY  241 AIGSGYLYKTTTFEKEVYSDLYGERGCLMGHGFIAQYEVLRERGHSPSEAFNEIVEEA 300
DB  241 AIGSGYLYKTTTFEKEVYSDLYGERGCLMGHGFIAQYEVLRERGHSPSEAFNEIVEEA 300
QY  301 TQSLYPLIGANGDMWTEACSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDGETQSRSL 360
DB  301 TQSLYPLIGANGDMWTEACSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDGETQSRSL 360
QY  361 DYNQSDPYREKYAEEMEIEIRNLEIWRAGKAVRSIRPENQK 400
DB  361 DYNQSDPYREKYAEEMEIEIRNLEIWRAGKAVRSIRPENQK 400

RESULT 2
ILV5_NEUCR
ID  ILV5_NEUCR STANDARD; PRT; 402 AA.
AC  P38674; Q7RVDS5; O8X019;
DT  01-FEB-1995 (Rel. 31, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE  (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacyl
DE  reductoisomerase).
GN  Name=ilv-2; ORFNames=B11H24.150, NCU03608;
OS  Neurospora crassa.
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC  Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX  NCBI_TaxID=5141;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.

```

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RX  MEDLINE=93013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;
RA  Sista H., Bowman B.;
RT  "Characterization of the ilv-2 gene from Neurospora crassa encoding
RT  alpha-keto-beta-hydroxyacyl reductoisomerase.";
RL  Gene 120:115-118(1992).
RN  [2]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=74-OR23-1A / FGSC 987;
RX  MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
RA  Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
RA  Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA  Schulte U.;
RT  "What's in the genome of a filamentous fungus? Analysis of the
RT  Neurospora genome sequence.";
RL  Nucleic Acids Res. 31:1944-1954(2003).
RN  [3]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=74-OR23-1A / FGSC 987;
RX  MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA  Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA  Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA  Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA  Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
RA  Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA  Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA  Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA  Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysellis M.,
RA  Mauceli E., Bielke C., Rudd S., Frisman D., Krystofova S.,
RA  Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA  Macino G., Catchside D.F.A., Li W., Pratt R.J., Osmari S.A.,
RA  DeSouza C.P., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA  Varden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA  Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA  Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT  "The genome sequence of the filamentous fungus Neurospora crassa.";
RL  Nature 422:859-868(2003).
CC  -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
CC  = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
CC  -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate +
CC  NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
CC  -1- COFACTOR: Magnesium.
CC  -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
CC  isoleucine from 2-oxobutanoate: step 2.
CC  -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
CC  from pyruvate: step 2.
CC  -1- SUBCELLULAR LOCATION: Mitochondrial.
CC  -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; M84189; AAB00797.1; -; Genomic DNA.
EMBL; AL670005; CAD21284.1; -; Genomic DNA.
EMBL; AABX01000270; EAA32099.1; -; Genomic DNA.
PIR; JCI428; JCI428.
HSP; QSHV22; LNP3.
DR  InterPro; IPR000506; ACh_isomrdctse.
DR  Pfam; PF01450; ILVC; 1.
DR  TIGRFAMs; TIGR00465; ilvC; 1.
KW  Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
KW  Magnesium; Mitochondrion; NADP; Oxidoreductase; Transl. peptide.
FT  TRANSIT 1 26 Mitochondrion (Potential).
FT  CHAIN 27 402 Ketol-acid reductoisomerase.
FT  NP BIND 90 99 NADP (Potential).
FT  ACT SITE 177 177 Potential.
FT  CONFLICT 358 358 T -> R (in Ref. 1).
FT  CONFLICT 392 393 Missing (in Ref. 1).
SQ  SEQUENCE 402 AA; 44623 MW; 246F795898D2A174 CRC64;

Query Match 89.8%; Score 1881; DB 1; Length 402;

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RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AACM01000419; EAA67345.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE      405 AA;  44908 MW;  61CGAF99723A33PA CRC64;

Query Match          88.9%;   Score 1861.5;  DB 2; Length 405;
Best Local Similarity 88.1%; Pred. No. 3.5e-125;
Matches 357; Conservative 23; Mismatches 20; Indels 5; Gaps

Qy    1 MSAGFSKALRPMARQLAT--PAVQRSSFY-AASSMVRA--TRKAAPVTQQOIRGVKTM
Db    1 MASENLSKALRGPARQLASAPVQRTFFVSARAARAVRACAVARPVASGFIQQOIRGVKTM
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy    56 DFIGHKEQWERADWPKEKLEFYFKDDTLTALIGYGSGHQGLNRDNGLNVIIGVRKDGG
Db    61 DFIGHKEDVVERADWPQEKLFVEYFNKDTLTALIGYGSGHQGLNRDNGLNVIIGVRKNG
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy   116 KSKDAVDQGWPCKULPEVDEAI SRGTVMNLLSDAAQSETWPALKPQITKGKTYLFSSH
Db   121 KSKDAEODGWAGKNLFVDVAIEGRGTTVMNLLSDAAQSETWTPAIKPQLVKGKTYLFSSH
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy   176 GPSVPFKDLTKVEVPTDVVVILCAPKGSRTVRSIFREGRGINSFAVYQDVTGAEEAKA
Db   181 GPSVPFKDLTKVEVPTDIVVILCAPKGSRTVRSIFREGRGINSFAVYQDVTGAEEAKA
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy   236 IALGVAIGSGYLKYKTTTFKEVYSDLYGERGCMLGGIHGMFLAQEYVLRRERHGPSPEAFNE

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QY	296	TVEEATQSLYPLIGANGDMWYEA	CTTARRGAIDWS	PRFKDALKP	VFNQLYDSVKD	GS			
Db	301	TVEEATQSLYPLIGANGDMWYEA	CTTARRGAIDWS	PKFKDALKP	VFNLSLYDAVKD	GS			
QY	356	TORSLDYNSQDPYRKYEA	MEIEIRNLEIWRAGKAV	RSLRPNQK	400				
Db	361	TKRSLEYSQDPYRKYEA	MEKEIRELEIWRAGKAV	RSLRPNQK	405				
RESULT 4									
Q4WYW4_ASPFU									
AC	Q4WYW4_ASPFU PRELIMINARY;			PRT;	508 AA.				
ID	Q4WYW4;								
DT	13-SEP-2005	(TReMBLrel. 31,	Created)						
DT	13-SEP-2005	(TReMBLrel. 31,	Last sequence update)						
DT	13-SEP-2005	(TReMBLrel. 31,	Last annotation update)						
DE	Ketol-acid reductoisomerase.								
GN	ORFNames=Afu3gl4490;								
OS	Aspergillus fumigatus Af293.								
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;								
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.								
NCBI	TaxID=330879;								
RN	[1] _TNAME;								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=Af293;								
RA	Nierman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,								
RA	Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,								
RA	Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,								
RA	Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,								
RA	Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,								
RA	Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,								
RA	Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,								
RA	Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,								
RA	Kumagai T., Lafton A., Katge J.-P., Li W., Lord A., Lu C.,								
RA	Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.								
RA	Mourya I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,								
RA	Pendava M.A., Perlea M., Price C., Pritchard B.L., Quail M.A.,								
RA	Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,								
RA	Reinhold H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.								
RA	Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,								
RA	Sanchez-Ferrero J.C., Saunders D., Seeger K., Smarek R., Smarek S.								


```

RX PubMed-15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaut J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382130; CAG80542.1; -; Genomic DNA.
DR GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ilvC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
DR Complete proteome.
KW SEQUENCE 398 AA; 44160 MW; C98CB87C9AF26F1 CRC64;

Query Match 75.5%; Score 1581.5; DB 2; Length 398;
Best Local Similarity 75.8%; Pred. No. 4.3e-105;
Matches 304; Conservative 44; Mismatches 46; Indels 7; Gaps 3;

Qy 1 MSARFSGKALRPMARQATPAVQRSSFVAASSMV--RATRKAAVAPTQOQIRGKVTMDFA 58
Db 1 MSARLFSTA-----SKQARAARAVATVTSASRSISMAATRPAPKLSAPAVARTIKTISFN 56

Qy 59 GHKEQ-VWERADWPKEKLEFFKDDTLALIGYSGQHGQGLNLRDNGNLNVIIGVRKDGKS 117
Db 57 GKEDEIVHERADWPQEKLLDYFKNDTLALIGYSGQHGQGLNLRDNGNLNVIIGVRKDGAS 116

Qy 118 WKDAVDQGVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSHG 177
Db 117 WKAQEDQGVPGKNLFDVNEAIGKGTIIMNLLSDAAQSETWPAKLPQITKGTLYFSHG 176

Qy 178 SPVFKDLTKVPTDVIDLCPKSGRTVRSFLFREGGINSFPAVYQDVTGEAEKAI 237
Db 177 SPVFKDLTKVETPADVDVILVAPKSGRTVRSFLFKEGGINSSAVVNDVTGKADKAVA 236

Qy 238 LGVAIGSGLYKTTTPEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETV 297
Db 237 LAIAGVGSGVYQTTTPEKEVRSGLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETV 296

Qy 298 EEATQSLYPLIGANGMDMMYEACSTTARRGALDWSPRFKDALKPFVNFQDVSVDGSETQ 357
Db 297 EEATQSLYPLIGKYGMDTMYDACSTTARRGALDWSPRFKDALKPFVNFQDVSVDGSETQ 356

Qy 358 RSLDYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSLRPEN 398
Db 357 RSLFNSQDYRAKFAELQDIRDLEIWRVGVKEVRKLRPEN 397

RESULT 7
Q6BLZ4 DEBHA PRELIMINARY; PRT; 399 AA.
ID Q6BLZ4 DEBHA
AC Q6BLZ4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similar to cal[1983]CallV5 Candida albicans CallV5 ketol-acid
DE reducto-isomerase.
GN OrderedLocustNames=DRHAQF10483;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.

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OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed-15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaut J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382138; CAG89118.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ilvC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
DR Complete proteome; Isomerase.
KW SEQUENCE 399 AA; 44352 MW; 53D67F203BD09113 CRC64;

Query Match 73.6%; Score 1542; DB 2; Length 399;
Best Local Similarity 74.2%; Pred. No. 2.9e-102;
Matches 299; Conservative 52; Mismatches 52; Indels 8; Gaps 3;

Qy 1 MSARFSGKALRPMARQATPAVQRSSFVAASSMVRAATR---KAAVAPTQOQIRGKVTMD 56
Db 1 MSIRNASIRMARVASNNA--AKQVASKRALSALANAARPVVARKSIAPA--AARGVKTIIN 56

Qy 57 FAGHQVWERADWPKEKLEFFKDDTLALIGYSGQHGQGLNLRDNGNLNVIIGVRKDGK 116
Db 57 FGMDIIVHERADWPKEKLEFFKNDTLALIGYSGQHGQGLNLRDNGNLNVIIGVRKOGA 116

Qy 117 SWKDAVDQGVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSHG 176
Db 117 SWKAAIEDGWPGENLFDVNEAIGKGTIIMNLLSDAAQSETWESIKPQTEGKTLFESHG 176

Qy 177 FSPVFKDLTKVPTDVIDLCPKSGRTVRSFLFREGGINSFPAVYQDVTGEAEKAI 236
Db 177 FSPVFKELTHVEPTTIDVILAAPKSGRTVRLTFKEGGINSSAVVNDVTGKAEKAI 236

Qy 237 ALGVAIGSGLYKTTTPEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNET 296
Db 237 ALAVAIGSGVYQTTTPEKEVSDLYGERGCLMGGIHGMFLAQYEVLRENGHTSEAFNET 296

Qy 297 VEEATQSLYPLIGANGMDMMYEACSTTARRGALDWSPRFKDALKPFVNFQDVSVDGSET 356
Db 297 VEEATQSLYPLIGKYGMDYMDACSTTARRGALDWSPRFKDALKPFVNFQDVSVDGSET 356

Qy 357 QRSIDYNSQDPYREKYAEEMEEIRNLEIWRAGKAVRSLRPENQ 399
Db 357 QRSIDYNSQSDYRAKFAELQDIRDLEIWRVGVKEVRKLRPENQ 399

RESULT 8
Q6C7Y1 KUJULA PRELIMINARY; PRT; 397 AA.
ID Q6C7Y1 KUJULA
AC Q6C7Y1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.

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GN	OrderedLocusNames=KLLA0A02673g;	DT	10-MAY-2005 (Tremblrel. 30, Last sequence update)
OS	Kluyveromyces lactis (Yeast).	DT	10-MAY-2005 (Tremblrel. 30, Last annotation update)
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	DE	Likely mitochondrial ketol-acid reductoisomerase.
OC	Saccharomycetales; Saccharomycetaceae; Kluyveromyces.	GN	Name=ILV5; ORFNames=Ca019.7733;
OX	NCBI_TaxID=28985;	OS	Candida albicans SC5314.
RN	[1]	OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	OC	Saccharomycetales; Mitosporic Saccharomycetales; Candida.
RC	STRAIN=CHS 2359 / IFO 1267 / NRRL Y-1140 / WM37;	OX	NCBI_TaxID=237561;
RX	PubMed=15229592; DOI=10.1038/nature02579;	RN	[1]
RA	Dufon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	RP	NUCLEOTIDE SEQUENCE.
RA	Lafontaine I., de Montigny J., Marek C., Neuveglise C., Talia E.,	RC	STRAIN=SC5314;
RA	Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,	RX	PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA	Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,	RA	Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA	Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,	RA	Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	RA	Davis R.W., Scherer S.,
RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,	RT	"The diploid genome sequence of Candida albicans.";
RA	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	RL	Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RA	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	RN	[2]
RA	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	RP	NUCLEOTIDE SEQUENCE.
RA	Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,	RC	STRAIN=SC5314;
RA	Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	RA	Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA	Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,	RA	Roberts J., Persson K., Donnelly S., Favoreto S., Izung K.-W.,
RA	Wincker P., Souciet J.-L.;	RA	Jones T., Scherer S., Agabian N.;
RT	"Genome evolution in yeasts.";	RT	"Annotation of the Genome of Candida albicans.";
RL	Nature 430:35-44 (2004).	RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; CR382121; CAH02706.1; -; Genomic DNA.	CC	-1- CAUTION: The sequence shown here is derived from an
DR	GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.	CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	CC	preliminary data.
DR	GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.	DR	EMBL; AACQ01000112; EAK94923.1; -; Genomic DNA.
DR	InterPro; IPR005056; ACh_isomrdctse.	KW	Isomerase.
DR	Pfam; PF01450; ILVC; 1.	SQ	SEQUENCE 400 AA; 44848 MW; ACD3162D05078D81 CRC64;
DR	TIGRFAMs; TIGR00465; ilvC; 1.	Query Match	72.9%; Score 1526.5; DB 2; Length 400;
KW	Complete proteome.	Best Local Similarity	73.8%; Pred. No. 3.8e-101;
SQ	SEQUENCE 397 AA; 44189 MW; 7634BEC037ABAA9B CRC64;	Matches 292; Conservative 41; Mismatches 55; Indels 6; Gaps 2;	
QY	11 RPARQL-----ATPAVQRSSFAAASMVRAATRAKAAVAPQ-QQIRGVKTMDFAGHKEOV 64	QY	1 MSAGFGSKALRPMARQATPAVQRSSFAA-ASSMVRAATRAKAAVAPQ-QQIRGVKTMDFAGHKEOV 58
DB	3 RQARQLIANSRVITAKRAISFAARQSTVSGLRSTAFASKPLVATRGIKQINFGVEETV 62	DB	1 MSFRITTSMEARLATAKATLSKRTFSLANATRYTAASSAAKAMTPITSIRGVKTINGF 60
QY	65 WERADPFKEKLEFYKDDTLALIGYSGQGGQGLNRDNLNVIIGVRKDGKSKDAVOD 124	QY	59 GHKEQWERADWPCKLLEYFKDDTLALIGYSGQGGQGLNRDNLNVIIGVRKDGKSKW 118
DB	63 YERADPFTEKLYFKDDTLALIGYSGQGGQGLNRDNLNVIIGVRKNGASWKAIED 122	DB	61 GTEEVVHERADWPCKRLLDYFKNDTFALITGYSGQGGQGLNRDNLNVIIGVRK-GSSW 119
QY	125 GWTPGKGLFVDEAISRGTIVMNLSDAAQSETWPAKPOITKGTLYFSHGSPVFKDL 184	QY	119 KDAVODGWPVGNLFEVDEAISRGTIVMNLSDAAQSETWPAKPOITKGTLYFSHGFS 178
DB	123 GWVPGENLFDVNEAVQKGTIVMNLSDAAQSETWSSLLKPLLTKGTLYFSHGSPVFKDL 182	DB	120 EAAVEDGWVPGENLFEVDEAISRGTIIMDLSDAAQSETWFFHKPQLTEGKTLFSHGFS 179
QY	185 TKVEVPTDVIILCAPKSGRTVRSIFREGRGINSSFAVYQDVYTGAEAEKAIAGVAGS 244	QY	179 PVFKDLTKVEVPTDVIILCAPKSGRTVRSIFREGRGINSSFAVYQDVYTGAEAEKAIAL 238
DB	183 THVEPPTDVIILVAPKSGRTVRSIFKEGRGINSSYAVVNDVYTGAEKAQALAVAGS 242	DB	180 PVFKDLTHVEPSPNDVILAAPKSGRTVRSIFKEGRGINSSYAVVNDVYTGAEKAIAM 239
QY	245 GYLTKTTFKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVETQSL 304	QY	239 GVAIGSGYLYKTTPEKVEYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 298
DB	243 GYVYQTTTFKEVNSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVETQSL 302	DB	240 AIAIGSGYVYKTTTFEVENSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 299
QY	305 YPLIGANGMDWMYEAESTTARRGAIDWSPRFKDALKPVFNQLYDVKDGETORSLDYNS 364	QY	299 EATQSLYPLIGANGMDWMYEAESTTARRGAIDWSPRFKDALKPVFNQLYDVKDGETOR 358
DB	303 YPLIGKGYMDYMDYDASTTARRGALDWMYPIFKDALKPVFDLYESTKNGSETKRSLEFNS 362	DB	300 EATQSLYPLIGKGYMDYMDYDASTTARRGALDWMYPIFKDALKPVFEELYEVKNGSETKR 359
QY	365 QPDYREKYAEEMEIRNLNLEIWRAGKAVRSIRLPEN 398	QY	359 SLDYNSQPDYREKYAEEMEIRNLNLEIWRAGKAVRSIRLPENQ 399
DB	363 QPDYREKLEAEQLIRNMEIWRKVEKVRKLRPEN 396	DB	360 SLEFNSRDYKERELEELQTIIRNMEIWRKVEKVRKLRPENQ 400
RESULT 9		RESULT 10	
Q59WR5 CANAL		Q59XR8 CANAL	
ID Q59WR5		ID Q59XR8	
AC Q59WR5		AC Q59XR8	
DT 10-MAY-2005 (Tremblrel. 30, Created)		DT 10-MAY-2005 (Tremblrel. 30, Created)	


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Db 6 SSRAMKALRTMGSRRLATRSMSVWART-TAAPSMRFPAPMTA---PLMQTRGMRVMDFA 61
QY 59 GHKEQVWERADWPKEKLELYFKDDTLALIGYSGHGGQGLNLRDNLNVIIGVRKDGKSW 118
Db 62 GTKENVWERSDWPKEKLVDFKNDTLAIIGYSGHGGQGLNARDQGLNVIIGVRKDGASW 121
QY 119 KOAVODGWVCKNLFEVDRAISRTVTIMNLLSDAAQSETWPALKPQITKTKTLYFSHGFS 178
Db 122 KOALEDGWVCKTLFFPVEEAIKGSIIMNLLSDAAQSETWPALKPQITKTKTLYFSHGFS 181
QY 179 PVFKDLTKVEVPTDVIDILCAPKSGSRTVRSFLFREGGINSFAVYQDVDTGEAEKAIAL 238
Db 182 VIFKQDKIHPKQDVIVLAPKSGSRTVRLFKEGGINSFAVYQDVDTGKAQEKALGL 241
QY 239 GVAIGSYLYKTTPEKEVYSDLYGERGCLMGHGMFLAQYVLRERGHSPSEAFNETVE 298
Db 242 AVAVGSGFIYQTTFKKEVYSDLYGERGCLMGHGMFLAQYVLRERGHSPSEAFNETVE 301
QY 299 EATQSLYPLIGANGMDWMYACSTTARRGAIDWSPRFKDALKPVPNQLYDSVKDGETOR 358
Db 302 EATQSLYPLIGKGLDYMFAACSTTARRGAIDWTPRFLEANKKVNLNELYDNVENGNEAKR 361
QY 359 SLDYNQSDPYREKYAEEMERINLEIWRAGKAVRSLRPENOK 400
Db 362 SLEYNAPNRYELDYKELEERINLEIWKAGEVVRSLRPEHNK 403
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RESULT 15
Q02340 YEAST
ID Q02340_YEAST PRELIMINARY; PRT; 395 AA.
AC Q02340;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acetohydroxy-acid isomeroreductase.
GN Names:ILV5G;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
RA Xie Q., Jimenez A.;
RT "Cloning and molecular analysis of two different ILV5 genes from a
RT brewing strain of Saccharomyces cerevisiae.";
RL Curr. Genet. 26:398-402(1994).
DR EMBL; S77495; AAB33578.1; -; Genomic_DNA.
DR HSSP; Q01292; IQMG.
DR Ensembl; YLR355C; Saccharomyces cerevisiae.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrctse.
DR Pfam; PF01450; ILV5; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
SQ SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2AEF CRC64;
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Query Match 71.1%; Score 1489; DB 2; Length 395;
Best Local Similarity 72.2%; Pred. No. 1.8e-98;
Matches 285; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

QY 10 LRPWAKQL---ATPAVORRSFVAASNVRAATRKAA--VAPTOQQQIRGVKTMDFAGHKEQV 64
Db 2 LRTQAAARLICNSRVWTKRTFALATRAAAYSRPAARFVKP-MVATRGLQKQINFGGTVETV 60
QY 65 WEADWPKEKLELYFKDDTLALIGYSGHGGQGLNLRDNLNVIIGVRKDGKSWKDAVD 124
Db 61 YERADWPKEKLELYFKDDTLALIGYSGHGGQGLNLRDNLNVIIGVRKDGASWKAIED 120
QY 125 GWVPGKNLFEVDRAISRTVTIMNLLSDAAQSETWPALKPQITKTKTLYFSHGFSPVFKDL 184
Db 121 GWVPGQNLFSVEDAIKKNYVMNLLSDAAQSETWPTIKPLTKTKTLYFSHGFSPVFKDL 180
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QY 185 TKVEVPTDVIDILCAPKSGSRTVRSFLFREGGINSFAVYQDVDTGEAEKAIALGVAIGS 244
Db 181 THVEPPKDLVIDILVAPKSGSRTVRSFLFKEGGINSFYAVNDVTGKAHEKAQALAIVAIGS 240
QY 245 GYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYVLRERGHSPSEAFNETVEEATQSL 304
Db 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYVLRERGHSPSEAFNETVEEATQSL 300
QY 305 YPLIGANGMDWMYACSTTARRGAIDWSPRFKDALKPVPNQLYDSVKDGETORSLDYN 364
Db 301 YPLIGKYGMDYWDACSTTARRGALDWYDFKNALKPVPQDIYESTKNGTETKRSLEFNS 360
QY 365 QPDYREKYAEEMERINLEIWRAGKAVRSLRPENQ 399
Db 361 QPDYREKLEKELVTIRNMEIWKVGEVRKLRPENK 395
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Search completed: March 22, 2006, 15:33:24
Job time : 127.94 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 123.747 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248A-2
Perfect score: 2071
Sequence: 1 MLRTQARLICNSRVITAKR.....RNMEIKVGVKLRPENC 395

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	1 ILV5 YEAST	P06168 saccharomyc
2	2066	99.8	395	2 Q02341 YEAST	Q02341 saccharomyc
3	2023	97.7	395	2 Q02340 YEAST	Q02340 saccharomyc
4	1903	91.9	399	2 Q6FXG6 CANGA	Q6FXG6 candida gla
5	1799	86.9	397	2 Q6CY71 KLULA	Q6CY71 kluyveromyc
6	1680	81.1	394	2 Q75CW4 ASHGO	Q75CW4 ashbva gos8
7	1667	80.5	400	2 Q59WV5 CANAL	Q59WV5 candida alb
8	1665	80.4	399	2 Q6BLZ4 DEBHA	Q6BLZ4 debaryomyc
9	1663	80.3	400	2 Q59XR8 CANAL	Q59XR8 candida alb
10	1582	76.4	398	2 Q6CAF8 YARLI	Q6CAF8 yarrowia li
11	1528.5	73.8	402	1 ILV5 NEUCR	P38674 neurospora
12	1507.5	72.8	405	2 Q4HY40 GIBZE	Q4HY40 gibberella
13	1507	72.8	400	2 Q52P28 WAGER	Q52P28 magnaporthe
14	1494.5	72.2	508	2 Q4WYW4 ASPFU	Q4WYW4 aspergillus
15	1477	71.3	400	2 Q5BAA4 EMENI	Q5BAA4 aspergillus
16	1467.5	70.9	404	1 ILV5 SCHPO	P78827 schizosacch
17	1401.5	67.7	401	2 Q55QW8 CRYNE	Q55QW8 cryptococcu
18	1401.5	67.7	401	2 Q55QW8 CRYNE	Q55QW8 cryptococcu
19	1383.5	66.8	401	2 Q96VZ5 CRYNE	Q96VZ5 cryptococcu
20	1256.5	60.7	625	2 Q4P572 USTWA	Q4P572 ustilago ma
21	1122	54.2	352	2 Q94135 PFUNG	Q94135 piromyces s
22	1107.5	53.5	362	2 Q5L9J3 BACFN	Q5L9J3 bacteroides
23	1101.5	53.2	359	2 Q8A612 BACTN	Q8A612 bacteroides
24	1099.5	53.1	347	2 Q64PT1 BACFR	Q64PT1 bacteroides
25	1038	50.1	344	2 Q84TR5 ASTYP	Q84TR5 aster yello
26	505	24.4	332	1 ILVC PYRFU	Q8u2a3 pyrococcus
27	495	23.9	332	1 ILVC PYRAB	Q9uz09 pyrococcus
28	485.5	23.4	333	1 ILVC AQUAE	Q67289 aquifex ao
29	484	23.4	330	1 ILVC METMP	Q612h4 methanococc
30	478	23.1	334	1 ILVC METJA	Q58938 methanococc
31	478	23.1	335	1 ILVC METAC	Q8tjj4 methanosarc

RESULT 1
ID ILV5 YEAST STANDARD; PRT; 395 AA.
AC P06168;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacyl reductoisomerase).
GN Name=ILV5; Ordered locus Names=YLK355C; ORFNames=L9638.7;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=87117524; PubMed=3027658;
RA Petersen J.G.L., Holmberg S.;
RT "The ILV5 gene of Saccharomyces cerevisiae is highly expressed."
RL Nucleic Acids Res. 14:9631-9651(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L.W., Riles L., Albertmann K., Andre B., Ansoorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hehling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [3]
RP PROTEIN SEQUENCE OF 166-174.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein database."
RT Electrophoresis 15:1466-1486(1994).
RN [4]
RP IDENTIFICATION OF PROBABLE N-TERMINUS.
RX MEDLINE=97121404; PubMed=8962070; DOI=10.1073/pnas.93.25.14440;
RA Shevchenko A., Jensen O.N., Podtelejnikov A.V., Sagliocco F., Wilm M., Vorm O., Mortensen P., Shevchenko A., Boucherie H., Mann M.;
RT "Linking genome and proteome by mass spectrometry: large-scale

Q8ztd1 pyrobaculum
Q97mV0 clostridium
Q92a29 listeria in
Q71y36 listeria mo
Q9uwx9 sulfobolus
Q9wz20 thermotoga
Q5kwj2 geobacillus
Q8p2z6 methanosarc
Q8r186 bacillus at
Q8y580 listeria mo
Q97la9 sulfobolus
Q73ba1 bacillus ce
Q63dx9 bacillus ce
P37253 bacillus su

32 473 22.8 328 1 ILVC PYRAE
33 470 22.7 337 1 ILVC CLOAB
34 468 22.6 331 1 ILVC LISIN
35 468 22.6 331 1 ILVC LISMF
36 468 22.6 335 1 ILVC SULSO
37 468 22.6 336 1 ILVC THEMA
38 467.5 22.6 341 2 Q5KWJ2 GEOKA
39 466 22.5 335 1 ILVC METMA
40 465.5 22.5 341 2 Q8RL86 BACST
41 465 22.5 331 1 ILVC LISMO
42 465 22.5 332 1 ILVC SULTO
43 461.5 22.3 336 1 ILVC BACCI
44 461.5 22.3 336 2 Q63DX9 BACCZ
45 461 22.3 342 1 ILVC BACSU

ALIGNMENTS

RT identification of yeast proteins from two dimensional gels.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445(1996).
 CC -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
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 CC -----
 CC EMBL; X04969; CAA28643.1; -; Genomic DNA.
 DR EMBL; U19102; AAB67753.1; -; Genomic_DNA.
 DR PIR; A24709; A24709.
 DR HSSP; Q01292; IQMG.
 DR IntAct; P06168; -.
 DR GERMOnline; 142419; -.
 DR SWISS-2DPAGE; P06168; YEAST.
 DR Ensembl; YLR355C; Saccharomyces cerevisiae.
 DR SGD; S00004347; ILV5.
 DR GO; GO:0042645; C:mitochondrial nucleoid; IDA.
 DR GO; GO:0005739; C:mitochondrion; IDA.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; TAS.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.
 DR GO; GO:0000002; P:mitochondrial genome maintenance; IMP.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; IlvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 DR Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
 KW Complete proteome; Direct protein sequencing; Magnesium;
 KW Mitochondrion; NADP; Oxidoreductase; Transit peptide.
 FT TRANSIT 1 47 Mitochondrion (Potential).
 FT CHAIN 48 395 NADP (Potential).
 FT NP BIND 84 93 NADP (Potential).
 FT REGION 363 395 Hydrophilic.
 FT ACT SITE 171 171 Potential.
 SQ SEQUENCE 395 AA; 44368 MW; D76419A6AD68E85E CRC64;
 Query Match 100.0%; Score 2071; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 2.1e-141;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB |||||
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB |||||
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQLNRDNLNVIIGVRKDGASWKAALIED 120
 DB |||||
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQLNRDNLNVIIGVRKDGASWKAALIED 120
 DB |||||
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB |||||
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 241 GYVYQTFEREVNSDLYGERGCLMGHGMFLAQDYDLVLRNGHSPSEAFNVEATQSL 300
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 241 GYVYQTFEREVNSDLYGERGCLMGHGMFLAQDYDLVLRNGHSPSEAFNVEATQSL 300
 DB |||||
 QY 301 YPLIGKGYGMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
 DB |||||
 QY 301 YPLIGKGYGMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
 DB |||||

Db 301 YPLIGKGYGMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
 QY 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 Db 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 RESULT 2
 Q02341_YEAST PRELIMINARY; PRT; 395 AA.
 ID Q02341_YEAST PRELIMINARY; PRT; 395 AA.
 AC Q02341;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acetohydroxy-acid isomerase.
 GN Names: ILV5; Synonyms: ILV5X;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
 RA Xie Q., Jimenez A.;
 RT "Cloning and molecular analysis of two different ILV5 genes from a
 RT brewing strain of Saccharomyces cerevisiae.";
 RL Curr. Genet. 26:398-402(1994).
 DR EMBL; S77496; AAB33579.1; -; Genomic_DNA.
 DR HSSP; Q01292; IQMG.
 DR Ensembl; YLR355C; Saccharomyces cerevisiae.
 DR SGD; S000004347; ILV5.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; IlvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 SQ SEQUENCE 395 AA; 44385 MW; D1D319A6A238E85E CRC64;
 Query Match 99.8%; Score 2066; DB 2; Length 395;
 Best Local Similarity 99.7%; Pred. No. 4.8e-141;
 Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB |||||
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB |||||
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQLNRDNLNVIIGVRKDGASWKAALIED 120
 DB |||||
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQLNRDNLNVIIGVRKDGASWKAALIED 120
 DB |||||
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB |||||
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 181 THVEPPKDLVLVAPKSGSRTVRSIFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB |||||
 QY 241 GYVYQTFEREVNSDLYGERGCLMGHGMFLAQDYDLVLRNGHSPSEAFNVEATQSL 300
 DB |||||
 QY 241 GYVYQTFEREVNSDLYGERGCLMGHGMFLAQDYDLVLRNGHSPSEAFNVEATQSL 300
 DB |||||
 QY 301 YPLIGKGYGMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
 DB |||||
 QY 301 YPLIGKGYGMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
 DB |||||
 QY 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 Db 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 RESULT 3
 Q02340_YEAST

Q02340_YEAST PRELIMINARY; PRT; 395 AA.
AC Q02340;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetohydroxy-acid isomeroreductase.
GN Name=ILV5G;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
RX Xie Q., Jimenez A.;
RT "Cloning and molecular analysis of two different ILV5 genes from a
RT brewing strain of Saccharomyces cerevisiae.";
RL Curr. Genet. 26:398-402(1994).
DR EMBL; S77495; AAB33578.1; -; Genomic_DNA.
DR HSSP; Q01292; 1QMG.
DR Ensembl; YLR355C; Saccharomyces cerevisiae.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ilvc; 1.
DR TIGRFAMs; TIGR00465; ilvc; 1.
SQ SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2ABF CRC64;

Query Match 97.7%; Score 2023; DB 2; Length 395;
Best Local Similarity 97.0%; Pred. No. 6.2e-138;
Matches 383; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAARFVKPMITRGLKQINFGGVETV 60
Db 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAARFVKPMITRGLKQINFGGVETV 60

Qy 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWKAIED 120
Db 61 YERADWPREKLLNFKDITFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWKAIED 120

Qy 121 GWVPKGLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGSPVPKDL 180
Db 121 GWVPKGLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGSPVPKDL 180

Qy 181 THVEPPKDLVDILVAPKSGRTVRSFLKEGSGINSSYAVVNDVTGKAHEKAQALAVAIGS 240
Db 181 THVEPPKDLVDILVAPKSGRTVRSFLKEGSGINSSYAVVNDVTGKAHEKAQALAVAIGS 240

Qy 241 GYVQTTFEREVNSDLGGERGLMGHGMFLAQYDVLRENGHSPSEAFNETVEATQSL 300
Db 241 GYVQTTFEREVNSDLGGERGLMGHGMFLAQYDVLRENGHSPSEAFNETVEATQSL 300

Qy 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVDLYESTKNGTETKRSLEFNS 360
Db 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVDLYESTKNGTETKRSLEFNS 360

Qy 361 QPDYREKLEKELDTIRNMEIKWVKEVRKLRPENQ 395
Db 361 QPDYREKLEKELDTIRNMEIKWVKEVRKLRPENK 395

RESULT 4
Q6FXG6_CANGA
ID Q6FXG6_CANGA PRELIMINARY; PRT; 399 AA.
AC Q6FXG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome B complete sequence.
GN OrderedLocNames=CAGL0B03047g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durkens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pelland S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Senouen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380948; CAG58005.1; -; Genomic DNA.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ilvc; 1.
DR TIGRFAMs; TIGR00465; ilvc; 1.
KW Complete proteome.
SQ SEQUENCE 399 AA; 44568 MW; E2241C86A034D728 CRC64;

Query Match 91.9%; Score 1903; DB 2; Length 399;
Best Local Similarity 89.5%; Pred. No. 3e-129;
Matches 358; Conservative 26; Mismatches 10; Indels 6; Gaps 2;

Qy 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAA-----RVKPMITRGLKQINFGG 55
Db 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAA-----RVKPMITRGLKQINFGG 55

Qy 56 TVETVYERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWK 115
Db 60 TVETVYERADWPREKLLNLFANDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWK 119

Qy 116 AATDGWPGKGLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGSP 175
Db 120 AATDGWPGKGLFTVEDAIKRGSYVMNLLSAAQSETWNSLKLTLTFSHGSP 179

Qy 176 VFQDLTHVEPPKDLVDILVAPKSGRTVRSFLKEGSGINSSYAVVNDVTGKAHEKAQALA 235
Db 180 VFQDLTHVEPPKDLVDILVAPKSGRTVRSFLKEGSGINSSYAVVNDVTGKAHEKAQALA 239

Qy 236 VAIGSGVYVQTTFEREVNSDLGGERGLMGHGMFLAQYDVLRENGHSPSEAFNETVEE 295
Db 240 VAVGSGVYVQTTFEREVNSDLGGERGLMGHGMFLAQYDVLRENGHSPSEAFNETVEE 299

Qy 296 ATQSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVDLYESTKNGTETKRS 355
Db 300 ATQSLYPLIGKGYMDYDACSTTARRGALDWYPIFKDALKPVDLYESTKNGTETKRS 359

Qy 356 LEFNSQPDYREKLEKELDTIRNMEIKWVKEVRKLRPENQ 395
Db 360 LEFNSQPDYREKLEKELDTIRNMEIKWVKEVRKLRPENQ 399

RESULT 5
Q6CY71_KUULA
ID Q6CY71_KUULA PRELIMINARY; PRT; 397 AA.
AC Q6CY71;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-1140 of Kluyveromyces lactis.

```

GN OrderedLocusNames=KLLA0A02673g;
OS Kluyveromyces lactis (Yeast);
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 /IFO 1267 /NRRL Y-1140 /WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neugebäude C., Tallia E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Henneguin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
RA Nicoud J.-M., Nikolski M., Orlas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382121; CAH02706.1; -; Genomic DNA.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
KW Complete proteome.
SQ SEQUENCE 397 AA; 44189 MW; 7634BEC037ABAA9B CRC64;

Query Match 86.9%; Score 1799; DB 2; Length 397;
Best Local Similarity 85.9%; Pred. No. 1e-121;
Matches 340; Conservative 23; Mismatches 31; Indels 2; Gaps 1;

QY 1 MLRTQAALICNSRVITAKETPALATFAAAYS--RPAARFVKPMITTRGLKQINFGTVE 58
DB 1 MFQQAARQLIANSRVITAKRAISFAARQSTVSLRSTAFASKPLVATRGIKQINFGVBE 60

QY 59 TVYERADWPREKLLDYFKNDTFALIGYSGQYQGLNLRDNLNGLNVIIGVRKDGASWKA 118
DB 61 TVYERADWPEKLLQYFKDDTLALIGYSGQYQGLNLRDNLNGLNVIIGVRKDGASWKA 120

QY 119 EDGWVPKGLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTFYSHGFSVPFK 178
DB 121 EDGWVPGENLFDVNEAVQKGTIVMNLSDAAQSETWSSLKPLLTGKTLTFYSHGFSVPFK 180

QY 179 DLTHVPPKDLVDILVAPKSGRTVRSFLFKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 238
DB 181 DLTHVPPPTDIDVILVAPKSGRTVRSFLFKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 240

QY 239 GSGYVYQTTFERVNSDLGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQ 298
DB 241 GSGYVYQTTFERVNSDLGERGCLMGHGMFLAQYEVILRENGHSPSEAFNETVEEATQ 300

QY 299 SLVPLIGKGYMDWYDACSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEF 358
DB 301 SLVPLIGKGYMDWYDACSTTARRGALDWYPIFKDALKPVFDLYSTKNGTETKRSLEF 360

QY 359 NSQPDYREKLEKLDITIRNMEIWKVKEVRKLRPEN 394
DB 361 NSQPDYREKLEAELQIRNMEIWKVKEVRKLRPEN 396

RESULT 6
Q75CW4 ASHGO
ID Q75CW4_ASHGO PRELIMINARY; PRT; 394 AA.
AC Q75CW4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)

us-10-797-248a-2.rup

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE ACL198Wp.
GN Name=ACL198W;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
Saccharomycetes cerevisiae genome.";
RL Science 304:304-307 (2004).
DR EMBL; AR016816; AAS51030.1; -; Genomic_DNA.
DR AGD; ACL198W; -.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
KW Complete proteome.
SQ SEQUENCE 394 AA; 43675 MW; 15A4E4FB942ACDA3 CRC64;

Query Match 81.1%; Score 1680; DB 2; Length 394;
Best Local Similarity 81.5%; Pred. No. 4.1e-113;
Matches 317; Conservative 32; Mismatches 28; Indels 12; Gaps 2;

QY 18 AKRTFALATRAAY-----SRPAARFVK-----PMITTRGLKQINFGTVEYERAD 65
DB 5 AGRQMIAGTRAAAWRALSGARARAAWPPVRSARAAAPLVQSGRGVKQISFGTPTTYERAD 64

QY 66 WPREKLLDYFKNDTFALIGYSGQYQGLNLRDNLNGLNVIIGVRKDGASWKAIEDGWVPG 125
DB 65 WPREKLLDYFKNDTFALIGYSGQYQGLNLRDNLNGLNVIIGVRKDGASWKAIEDGWVPG 124

QY 126 KNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTFYSHGFSVPFKDLTHVEP 185
DB 125 ENLFDVNEAVRGTTVMNLLSDAAQSETWPTPLLTGKTLTFYSHGFSVPFKDLTHVEP 184

QY 186 PKDLVDILVAPKSGRTVRSFLFKEGRGINSSYAVVNDVTGKAHEKAQALAVAI GSGYVYQ 245
DB 185 PKDLVDILVAPKSGRTVRSFLFKEGRGINSSYAVVNDVTGKAHEKAQALAVAI GSGYVYQ 244

QY 246 TTFEREVNSDLGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLIG 305
DB 245 TTFEREVNSDLGERGCLMGHGMFLAQYEVILRENGHSPSEAFNETVEEATQSLYPLIG 304

QY 306 KYGMDYMDYDACSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFN SQPDYR 365
DB 305 KHGMDYMDYDACSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFN SQPDYR 364

QY 366 EKLEKLDITIRNMEIWKVKEVRKLRPEN 394
DB 365 DKLEAELQIRNMEIWKVKEVRKLRPEN 393

RESULT 7
Q59WWS CANAL
ID Q59WWS CANAL PRELIMINARY; PRT; 400 AA.
AC Q59WWS;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Likely mitochondrial ketol-acid reductoisomerase.
GN Name=ILV5; ORFNames=CaO19.7733;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.

[1]
NCBI_TaxID=237561;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA DuJong B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Swennen D., Tekala F., Wesolowski-Louvet M., Westhof E., Wirth B.,
Zenou-Neyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincher P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382138; CAG89118.1; -; Genomic DNA.
DR GO; GO:0016853; F-isomerase activity; IEA.
DR GO; GO:0004455; F-ketol-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P-branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctase.
DR PFam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvc; 1.
KW Complete proteome; Isomerase.
SQ SEQUENCE 399 AA; 44352 MW; 53D67F203BD09113 CRC64;

Query Match 80.4%; Score 1665; DB 2; Length 399;
Best Local Similarity 80.3%; Pred. No. 5e-112;
Matches 317; Conservative 29; Mismatches 41; Indels 8; Gaps 1

QY 1 MURTOARLINCNSRVITAKRTFALATRAAAYSRPAARFVKMTTRGLKQINFGTIVT 60
DB 13 MASNNAAQVASKRALSALANAAPVAVKSTAPAA-----ARGVKTINFGMDIV 64

QY 61 YERADWPBKLDYFKNDFALIGYSGYGGGLNRDLNGLNVIIGVRKDGASWKAATED 120
DB 65 HERADWPBKLEYFKNDFALIGYSGYGGGLNRDLNGLNVIIGVRKDGASWKAATED 124

QY 121 GWVPKGNLFTVBDIAIKRGSYVNNLLSDAAQSETWPAIKPLLTGKTLFSGHGFSPVKDL 180
DB 125 GWVPKGNLFTVBDIAIKRGSYVNNLLSDAAQSETWPAIKPLLTGKTLFSGHGFSPVKDL 184

QY 181 THVEPPKLDVLIVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVAIGS 240
DB 185 THVEPPKLDVLIVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVAIGS 244

QY 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQVDVLRNENGHPSEAFNFTVEATOSL 300
DB 245 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQVDVLRNENGHPSEAFNFTVEATOSL 304

QY 301 YPLIGKGYMDYMDACSTTARRGALDWYPIFNALKPVFDLYESTKNGTETKRSLEFNS 360
DB 305 YPLIGKGYMDYMDACSTTARRGALDWYPIFNALKPVFDLYESTKNGTETKRSLEFNS 364

QY 361 QPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 395
DB 365 QPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 399

RESULT 9
Q59XR8_CANAL PRELIMINARY; PRT; 400 AA.
ID Q59XR8_CANAL PRELIMINARY;
AC Q59XR8;
DT 10-MAY-2005 (TremBLrel. 30, Created)
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE Likely mitochondrial ketol-acid reductoisomerase.
GN Names=ILV5; ORFNames=Cao19.88;
OS Candida albicans SC5314.

Saccharomycetales; mitosporic Saccharomycetales; Candida.

[1]
NCBI_TaxID=237561;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA DuJong B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Swennen D., Tekala F., Wesolowski-Louvet M., Westhof E., Wirth B.,
Zenou-Neyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincher P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382138; CAG89118.1; -; Genomic DNA.
DR GO; GO:0016853; F-isomerase activity; IEA.
DR GO; GO:0004455; F-ketol-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P-branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctase.
DR PFam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvc; 1.
KW Complete proteome; Isomerase.
SQ SEQUENCE 399 AA; 44352 MW; 53D67F203BD09113 CRC64;

Query Match 80.5%; Score 1667; DB 2; Length 400;
Best Local Similarity 79.1%; Pred. No. 3.6e-112;
Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;

QY 3 RTQARL--ICNSRVITAKRTFALATRAAAYSRPAARFVKMTTRGLKQINFGTV 57
DB 4 RTTSMARLATAKATLSKRTFSLANATTRYTAASSAAKAMTPTSIRGVKTNFGTGE 63

QY 58 ETVYERADWPBKLDYFKNDFALIGYSGYGGGLNRDLNGLNVIIGVRKDGASWKA 117
DB 64 EVYHERADWPBKLDYFKNDFALIGYSGYGGGLNRDLNGLNVIIGVRK-GSSWEAA 122

QY 118 IDGWPVGNLFTVBDIAIKRGSYVNNLLSDAAQSETWPAIKPLLTGKTLFSGHGFSPVF 177
DB 123 VEDGWVGNLFTVBDIAIKRGSYVNNLLSDAAQSETWPAIKPLLTGKTLFSGHGFSPVF 182

QY 178 KDLTHVEPPKLDVLIVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVA 237
DB 183 KDLTHVEPPKLDVLIVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVA 242

QY 238 ICSGYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQVDVLRNENGHPSEAFNFTVEAT 297
DB 243 ICSGYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQVDVLRNENGHPSEAFNFTVEAT 302

QY 298 QSLYPLIGKGYMDYMDACSTTARRGALDWYPIFNALKPVFDLYESTKNGTETKRSLE 357
DB 303 QSLYPLIGKGYMDYMDACSTTARRGALDWYPIFNALKPVFDLYESTKNGTETKRSLE 362

QY 358 FNSQPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 395
DB 363 FNSQPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 400

RESULT 8
Q6BLZ4_DEBHA PRELIMINARY; PRT; 399 AA.
ID Q6BLZ4_DEBHA PRELIMINARY;
AC Q6BLZ4;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Similar to ca[CAL1983]Candida albicans CAILV5 ketol-acid reductoisomerase.
GN OrderedLocusNames=DEHA0F10483g;
OS Debaryomyces Hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
NCBI_TaxID=4959;

RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=ATCC 36239 / CBS 767;
RX	PubMed=15229592; DOI=10.1038/nature02579;
RA	Dujon B., Sherman D., Montigny J., Marck C., Durrens P., Casaregola S.,
RA	Lafontaine I., de Montigny J., Aigle M., Anthouard V., Babour A., Barbe E.,
RA	Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA	Barnay S., Blanchin S., Beckerich J.-J., Boyne E., Bleykasten C.,
RA	Boisrame A., Boyer J., Cattolico L., Confanioli F., de Darovar A.,
RA	Deapons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA	Hanraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA	Kerrest A., Koszul K., Lemaire M., Lesur I., Ma L., Muller H.,
RA	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA	Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA	Svennen D., Tekala P., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA	Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA	Boucher C., Caudron B., ScarPELLI C., Gaillardin C., Weissenbach J.,
RA	Wincker P., Souciet J.-L.;
RT	"Genome evolution in yeasts";
RL	Nature 430:35-44(2004).
DR	ENBL; CR382138; CAG89118.1; -; Genomic DNA.
DR	GO; GO:0016853; F-isomerase activity; IEA.
DR	GO; GO:0004455; F-ketol-acid reductoisomerase activity; IEA.
DR	GO; GO:0009082; P-branched chain fatty amino acid biosynthesis; IEA.
DR	InterPro; IPRO00506; Ach isomrdtase.
DR	pfam; PF01450; IlvC; 1.
DR	TIGRFAMs; TIGR00465; ilvC; 1.
KW	Complete proteome; Isomerase.
SQ	SEQUENCE 399 AA; 44352 MW; 53D67F203BD09113 CRC64;
	Query Match 80.4%; Score 1665; DB 2; Length 399;
	Best Local Similarity 80.3%; Pred. No. 5e-112;
	Matches 317; Conservative 29; Mismatches 41; Indels 8; Gaps 1
Qy	1 MLTQTARALICNSRVITAKTFPALATAAAAYSPRARPFVKPMITTGLKQLINFGGTVETV 60
Db	13 MAGSNAKVASKRALASLANAAPVPVARKSIAPAA-----ARGVKTIINFGGMDSEIV 64
	:
Qy	61 YERADWPREKLDDYFKNDTEPALLCYGSQGYYGGNLNRDNLNVTIGVRKGDSWKAAATED 120
Db	65 HERADWPREKLDEYFNKDNTUALLGYSGQQYGQGNLRDNLNVTIGVRKGDSWKAAATED 124
	:
Qy	121 GWYPGKNLFVEDAIKRGSYVMNLLSDAAQSSTWPAIKPLLTGKTLYFSHGFSFPVKDL 180
Db	125 GWYPGENLPDVNEAIGKTYIMNLLSDAAQSSTWESIKPOLTEGKTLIFSFGFSFPVKEL 184
	:
Qy	181 THVEPPKDLVLILVAPKGSORTVRSFLPKGEGRGINSSAVNVNDVTGKAHKAQAALAIVAIGS 240
Db	185 THVEPTTNIDVILAAPKGSORTVRTLPKEGRGINSSAVNVNDVTGKAHKAQAALAIVAIGS 244
	:
Qy	241 GVVYTFTFEVNVDLYGERGCLMGGHGMFLAQDYLVLRNGHSPSFAFNETVEEATQSL 300
Db	245 GVVYTFTFEVNVDLYGERGCLMGGHGMFLAQEVLRNGHTTPSFANFETVEEATQSL 304
	:
Qy	301 YPLIGKYGDYMYDACSTARRGALDWYPIFKNALKEVFPOOLYESTKNGTETTKKSLEBENS 360
Db	305 YPLIGKYGDYMYDACSTARRGALDWYPRFDKALKPVENDLVESVNGTETQRSLDENIS 364
	:
Qy	361 QPYDKRKLEKELDTIRNMEIWVGKGVKVRKLKPENQ 395
Db	365 QSDYRARLEELETIRSMEIWRVWGKVRKLKPENQ 399
	:
RESULT 9	
Q59XR8 CANAL	
ID	Q59XR8 CANAL PRELIMINARY; PRT; 400 AA.
AC	Q59XR8;
DT	10-MAY-2005 (TrEMBLrel. 30, Created)
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE	Likely mitochondrial ketol-acid reductoisomerase.
GN	Name=ILV5; ORFName=Cao19_88;
OS	Candida albicans SC5314.

FT	CHAIN	27	402	Ketol-acid reductoisomerase.
FT	NP BIND	90	99	NADP (Potential).
FT	ACT SITE	177	177	Potential
FT	CONFLICT	358	358	T->R (in Ref. 1).
FT	CONFLICT	392	393	Missing (in Ref. 1).
FT	SEQUENCE	402 AA;	44623 MW;	246F795898D2A174 CRC64;
Query Match				
Best Local Similarity 74.1%; Score 1528.5; DB 1; Length 402;				
~Matches 297; Conservative 39; Mismatches 50; Indels 15; Gaps 4				
QY	4	TOAARLINCNSRVITA--KRTF--ALATRAA----	AYSRAARFVKPMITTRGLKQINFG	54
DB	7	TKALRPLARQLATPAVQRRTFVAASAVRASVAVKAVAAPARQOV-----	RGVKTMDFA	60
QY	55	GTIVTVTERADWPPEKLLDYFKNDTFALTYGSGOGVGGNLNRDNLGLNVI	IGVRKDGASW	114
DB	61	GKHEVHERADWPAEKLLDYFKNDTTLALTYGSGOGHGGNLNRDNLGLNVI	IGVRKNGKSW	120
QY	115	KAAIEDGWPVCKNLFYVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLFYSHGFS	174	
DB	121	EDAIDGWPVCKNLFYDEAIKRGTYVMNLLSDAAQSETWPHIKQITKGKTLFYSHGFS	180	
QY	175	PVFKDLTHVPPKDLVDILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHKAQAL	234	
DB	181	PVFKDLTKVEPTDVIDVILVAPKSGRTVRSFLFKEGRGINSFVAVVDVTGKAHKAQAL	240	
QY	235	AVATGSGYVQTTFERVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVE	294	
DB	241	GVAVGSGLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE	300	
QY	295	EATOSLPLIGKYGMDVYDACSTTARRGALDWYPIFKNALKVPQDLVYESTKNGCTETKR	354	
DB	301	EATOSLPLIGAGMDWMFACSTTARRAIDMTWPKDALKVPFNLLVDSVNGDETKR	360	
QY	355	SLEFNSQPDYREKLEKELDTIRNMEIWKVGKVRKLRPNQ	395	
DB	361	SLEFNSQPDYRERYEAELDIRNLETWRAKAVSLRPNQ	401	
RESULT 12				
Q4HY40 GIBZE PRELIMINARY; PRT; 405 AA.				
QAC	Q4HY40			
DT	13-SEP-2005	(TrEMBLrel. 31, Created)		
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)		
DE	ILV5_NEUCR	Ketol-acid reductoisomerase, mitochondrial (Acetohydroxy-		
DE	acid reductoisomerase)	(Alpha-keto-beta-hydroxylacil		
GN	ORFNames=FG10118.1;			
OS	Gibberella zeae PH-1.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocorymbicidae; Hypocreales; Nectriaceae; Gibberella.			
OX	NCBI_TaxID=229533;			
RN	[1]			
RRP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=PH-1;			
RA	Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,			
RA	Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,			
RA	Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,			
RA	Choepl Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,			
RA	Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engel R.,			
RA	Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,			
RA	Gardyna S., Gnerre S., Graham L., Gordon-Pierre N., Hafez N.,			
RA	Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,			
RA	Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,			
RA	Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,			
RA	Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,			
RA	Mathews C., Maucelli E., McCarthy M., Meldrum J., Meneus L.,			
RA	Mihova T., Miengua V., Murphy T., Naylor J., Nguyen C., Nicol R.,			
RA	Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,			
RA	Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,			

QY 241 GVVYQTFPERVNSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNFTVEATQSL 300
 DB 245 GYLKXTFEKEVYSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNFTVEATQSL 304
 QY 301 YPLIKGYMDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKKSLEFNS 360
 DB 305 YPLIGANGMDWYEAACSTTARRGALDWSPRFDKALKPVFQDLYSVKDSQTSQSLDYSN 364
 QY 361 QPDYREKLEKELDIRNMEIWKVKEVRLRPENQ 395
 DB 365 QPDYREKYEAEEMERINLEIWRAGKAVRSLRPENQ 399

RESULT 14
 Q4WY4 ASPFU
 ID Q4WY4 ASPFU PRELIMINARY; PRT; 508 AA.
 AC Q4WY4;
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Ketol-acid reductoisomerase.
 GN ORFNames=Afu3g14490;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley.
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Humphrey S., Jimenez J.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Whilliam R., Haas B.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Lage J.-F., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Palvela M.A., Partea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Ruter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
 RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.,
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.",
 RT Aspergillus fumigatus.",
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAHP01000002; EAL92139.1; -; Genomic_DNA.
 DR EMBL; AAHP01000002; EAL92139.1; -; Genomic_DNA.
 KW isomerase.
 SQ SEQUENCE 508 AA; 56353 MW; 09C99AB04D9D92BC CRC64;
 Query Match 72.2%; Score 1494.5; DB 2; Length 508;
 Best Local Similarity 71.9%; Pred. No. 1.5e-99;
 Matches 281; Conservative 46; Mismatches 61; Indels 3; Gaps 1;
 QY 5 QARALICNSRVITAKRTFFALATRAAAYSRPAARFVKPMITTRGLKQINFGTGVETVYERA 64
 DB 120 RALRL---ARVAAPRTVISAALPRPALAKAATRAAATAVPVGVKTIAPADSKETVYERA 176
 QY 65 DWPEKLLDYKNDTFALIGYSGYCGQLNRDNLNGLNVIYVRKOGASKAAIEDGWVP 124
 DB 177 DWPEKLEQYFKNDTLALIGYSGYCGQLNRDNLNGLNVIYVRKOGASKAAIQDGWIP 236
 QY 125 GKNLFTVEDAKRGSYVYNLLSDAAQSETWPAIKPLITKGLTYFSHGSPVFKDLTHVE 184
 DB 237 GKNLFDITEAVQKRTIYNLLSDAAQSETWPTLKLITKGLTYFSHGSPVFKELTKVD 296

QY 185 PPKDLVDILVAPKSGRTVRSFLFKBGRGINSSVAVNDVTGKAHEKAQALAVAGSYVY 244
 DB 297 VPKDVVDILVAPKSGRTVRSFLFKBGRGINSSVAVNDVTGKAHEKAQALAVAGSYVY 356
 QY 245 QTTFERVNSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNFTVEATQSLYPLI 304
 DB 357 ETTFEKEVYSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNFTVEATQSLYPLI 416
 QY 305 GKYGMIDYMDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKKSLEFNSQPDY 364
 DB 417 GANGMDWYEAACSTTARRGALDWSPRFDKALKPVFQDLYSVKDSQTSQSLYPLI 476
 QY 365 REKLEKELDIRNMEIWKVKEVRLRPENQ 395
 DB 477 REKYEKEMQDIRDLEIWRAGKAVRSLRPENQ 507

RESULT 15
 QSBAA4 EMENI
 ID QSBAA4 EMENI PRELIMINARY; PRT; 400 AA.
 AC QSBAA4;
 DT 10-MAY-2005 (Tremblrel. 30, Created)
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
 DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN2526.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryotes; Trichocomaceae; Emericella.
 OC NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguvalakiy L.,
 RA Boukagater B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli B., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.,
 RT "Genome Sequence of Aspergillus nidulans.",
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AACD01000043; EAA64631.1; -; Genomic DNA.
 DR GO; GO:0004455; F-ketol-acid reductoisomerase activity; IEA.
 DR GO; GO:0016491; F-oxidoreductase activity; IEA.
 DR GO; GO:0009082; P-branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomrctase.
 DR TIGRfam; TIGR00465; ilvc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
 Query Match 71.3%; Score 1477; DB 2; Length 400;
 Best Local Similarity 71.1%; Pred. No. 2e-98;
 Matches 278; Conservative 49; Mismatches 62; Indels 2; Gaps 1;

QY 5 QARALICNSRVITAKRTFFALATRAAAYSRPAARFVKPMITTRGLKQINFGTGVETVYERA 64

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 125.313 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248A-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRKRSIRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2069	99.2	402	1	ILV5_NEUCR
2	1860	89.2	400	2	Q52F28_MAGGR
3	1819.5	87.2	400	2	Q4HY40_GIBZE
4	1639	78.6	508	2	Q4WY4 ASPFU
5	1611	77.2	400	2	Q5BAA4_EWENI
6	1560.5	74.8	398	2	Q6CAP8_YARLI
7	1542	73.9	399	2	Q6BLZ4_DEBHA
8	1539.5	73.8	400	2	Q59MW5_CANAL
9	1535.5	73.6	400	2	Q59XR8_CANAL
10	1524	73.1	397	2	Q6CV71_KLULA
11	1508.5	72.3	395	1	ILV5_YEAST
12	1506.5	72.2	395	2	Q02341_YEAST
13	1500.5	71.9	399	2	Q6FKG6_CANGA
14	1494.5	71.6	404	1	ILV5_SCHPO
15	1479.5	70.9	395	2	Q02340_YEAST
16	1466.5	70.3	394	2	Q75CW4_ASHGO
17	1434.5	68.8	401	2	Q5KOW8_CRYNE
18	1434.5	68.8	401	2	Q5KOA0_CRYNE
19	1417.5	68.0	401	2	Q96VZ5_CRYNE
20	1232	59.1	625	2	Q4P572_USTWA
21	1099	52.7	352	2	Q94135_PFUNG
22	1086.5	52.0	362	2	Q5L9J3_BACFN
23	1084.5	52.1	347	2	Q64PT1_BACFR
24	1075.5	51.6	359	2	Q8A612_EACTN
25	1071	51.3	344	2	Q847R5_ASTYP
26	510.5	24.5	341	2	Q5KRW2_GEOKA
27	507.5	24.3	341	2	Q8RL86_BACST
28	497	23.8	333	1	ILV5_AQUAE
29	492	23.6	332	1	ILV5_PPRAB
30	485	23.3	332	1	ILV5_PPRAB
31	484.5	23.2	331	1	ILV5_LISIN

32	484.5	23.2	331	1	ILV5_LISMP
33	483	23.2	342	1	ILV5_BACSU
34	480.5	23.0	331	1	ILV5_LISMO
35	472.5	22.7	326	1	ILV5_METKA
36	470	22.5	335	1	ILV5_METAC
37	470	22.5	342	2	Q65GF7_BACLD
38	469.5	22.5	581	1	ILV5_PEA
39	469	22.5	328	1	ILV5_PYRAE
40	469	22.5	332	1	ILV5_GLOVI
41	466	22.3	578	2	Q65XK0_ORYSA
42	465	22.3	591	1	ILV5_ARATH
43	463	22.2	335	1	ILV5I_SULSO
44	463	22.2	337	1	ILV5I_CIOAB
45	463	22.2	341	2	Q5WEN2_BACSK

RESULT 1

ILV5_NEUCR STANDARD; PRT; 402 AA.
AC P38674; Q7RVD5; Q8X019;
DT 01-FEB-1995 (Rel. 31, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
GN Name=ilv-2; ORFNames=B11H24.150, NCU03608;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;
RA Sista H.; Bowman B.;
RT "Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxylacil reductoisomerase.";
RL Gene 120:115-118(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Altmann V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.";
RL Nucleic Acids Res. 31:1944-1954(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kanvasekalis M.,
Rasmussen C., Mettenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
Macino G., Catchside D.E.A., Li W., Pratt R.J., Osmari S.A.,
deSouza C.P.C., Glass N.I., Orbach M.J., Berglund J.A., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC -!- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)

ALIGNMENTS

CC = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate +
 CC NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
 CC isoleucine from 2-oxobutanoate; step 2.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
 CC from pyruvate; step 2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; M84189; AAB00797.1; -; Genomic DNA.
 DR EMBL; AL670005; CAD21284.1; -; Genomic DNA.
 DR EMBL; ABX01000270; EAA32099.1; -; Genomic DNA.
 DR PIR; JC1428; JCI428.
 DR HSSP; O9HVA2; 1NP3.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; ilvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 KW Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
 KW Magnesium; Mitochondrion; NADP; Oxidoreductase; Transient peptide.
 FT TRANSIT 1 26 Mitochondrion (Potential).
 FT CHAIN 27 402 Ketol-acid reductoisomerase.
 FT NP_BIND 90 99 NADP (potential).
 FT ACT_SITE 177 177 Potential.
 FT CONFLICT 358 358 T -> R (in Ref. 1).
 FT CONFLICT 392 393 Missing (in Ref. 1).
 FT SEQUENCE 402 AA; 44623 MW; 2467795898D2A174 CRC64;
 Query Match 99.2%; Score 2069; DB 1; Length 402;
 Best Local Similarity 99.3%; Pred. No. 3e-138;
 Matches 399; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
 QY 1 MAARNCTKALPLARQLATPAVORRTFVAASAVRASVAVKAAAPARQVRGVTMDFA 60
 Db 1 MAARNCTKALPLARQLATPAVORRTFVAASAVRASVAVKAAAPARQVRGVTMDFA 60
 QY 61 GHKEEVEHRAADWPAEKLLDYFKNDTLALGYSGQHGQGLNRDNLNIVGVKNGKSW 120
 Db 61 GHKEEVEHRAADWPAEKLLDYFKNDTLALGYSGQHGQGLNRDNLNIVGVKNGKSW 120
 QY 121 EDIAQDGWPGKMLFDVDESAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLFSGHPS 180
 Db 121 EDIAQDGWPGKMLFDVDESAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLFSGHPS 180
 QY 181 PVFKDLTKVEPTDVIDVILVAPKSGRTVRSIPREGRGINSFVAVYQDVTGKAKEKAVAL 240
 Db 181 PVFKDLTKVEPTDVIDVILVAPKSGRTVRSIPREGRGINSFVAVYQDVTGKAKEKAVAL 240
 QY 241 GVAVSGYLITYETTFEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHSPGEAFNETVE 300
 Db 241 GVAVSGYLITYETTFEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHSPGEAFNETVE 300
 QY 301 EATQSLYPLIGAHGMDMWFACSTTARRGAIDWTPKFKDALKPVPFNLYDSVKNRGERDKR 360
 Db 301 EATQSLYPLIGAHGMDMWFACSTTARRGAIDWTPKFKDALKPVPFNLYDSVKNRGERDKR 360
 QY 361 SLEYNQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
 Db 361 SLEYNQPDYRERYEAELEIRNLEIWRAGKAVRSLRPENQK 402
 RESULT 2
 Q52F28_MAGGR
 ID Q52F28_MAGGR PRELIMINARY; PRT; 400 AA.
 AC Q52F28;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG01808.4; 70-15.
 OS Magnaporthe grisea
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=242507;
 RN [1]_ NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Duples A., Elkins T., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Duffey N., Duples A., Elkins T., Dorje P.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Engels R.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Glinka A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe T., Jones C., Kamal M., Kamat A., Kamvyselis M., Karlsson E.,
 RA Kellis C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Maucelli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mezes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan B., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer J., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuang P.,
 RA Tensing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Tsanla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACU01000121; EAA56157.1; -; Genomic DNA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR InterPro; IPR009014; Transketo_C-like.
 DR Pfam; PF01450; ilvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 400 AA; 44723 MW; 4C99B9E1495B6D75 CRC64;
 Query Match 89.2%; Score 1860; DB 2; Length 400;

[illegible]

RESULT 4	
ID Q4WYV4 ASPFU PRELIMINARY;	PRT; 508 AA.
AC Q4WYV4;	
AD Q4WYV4;	
DT 13-SEP-2005 (T=EMBLrel. 31, Created)	
DT 13-SEP-2005 (T=EMBLrel. 31, Last sequence update)	
DT 13-SEP-2005 (T=EMBLrel. 31, Last annotation update)	
DE Ketol-acid reductoisomerase.	
GN ORFNames=Afu3g14490;	
GO Aspergillus fumigatus Af293.	
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;	
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.	
OX NCBI_TaxID=330879;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=Af293;	
RA Nicrman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley,	
RA Arroyo J., Bezirram M., Abe K., Archer D.B., Bermejo C., Bennett J.,	
RA Bowyer P., Chen D., Collins M., Coulsein R., Davies R., Dyer P.S.,	
RA Farman M., Fedorova N., Fedorova N., Feildblyum T.V., Fischer R.,	
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,	
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,	
RA Haas H., Harris D., Horuchi H., Huang J., Humphrey S., Jimenez J.,	
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,	
RA Kumagai T., Lafton A., Katze J.-P., Li W., Lord A., Lu C.,	
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,	
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,	
RA Penalta M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,	
RA Rabinowitzsch E., Rawlins N., Rajandream M.-A., Reichard U.,	
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,	
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,	
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares P., Squares S.	

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RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Bartlett B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAHF01000002; EAL92139.1; -; Genomic_DNA.
KW isomerase.
SQ SEQUENCE 508 AA; 56353 MW; 09C99AB04D9D92EC CRC64;
Query Match 78.6%; Score 1639; DB 2; Length 508;
Best Local Similarity 78.8%; Pred. No. 1.2e-107;
Matches 320; Conservative 35; Mismatches 35; Indels 16; Gaps 6;
QY 1 MAARNCTKALRPLARQLATPAVQRFTFAA-----SAVRASVAVKAVAPARQVRGVKT 56
DB 113 MASRGLPRALR-LAR-VAAP-RTVISAALPRPALAKAATRAAATAP-VRGVKT 162
QY 57 MDPAGHKEEVRADWPAEKLDDYFKNDTLALIGYSGQHGQGLNLDNGLNVIIVGRKN 116
DB 163 IAFADSKETVIERADWPKEKLQYFKNDTLALIGYSGQHGQGLNLDQGLNVIIVGRKD 222
QY 117 GKSWEIDAIDGWVPGKKNLFDVDEAISRGITVMNLLSDAAQSETWPHIKPQITKGKTLYFS 176
DB 223 GASWKEAIDQGWIPGKKNLFDLTEAVQKGTVMNLLSDAAQSETWPTLKPIITGKTLYFS 282
QY 177 HGPSVPFKLTKEVPTDNDVILVAPKSGRTVRSILFRGGRGINSFAVYQDVTGKAKEK 236
DB 283 HGPSVPFKELTKVDVDPKVDVILVAPKSGRTVRTLFRGGRGINSIAVYQDVTGKAKEK 342
QY 237 AVALGVAVSGYLTYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 296
DB 343 AIAMGVAVSGYLTYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 402
QY 297 ETVEEATQSLYPLIGAHGMDWDFDACSITARRGAIDWTPKFKDALKPVFNLLYDSVKNGD 356
DB 403 ETVEEATQSLYPLIGANGDMWYAACTTARRGAIDWSRFRKDTLKPIFNELYDSVRDGT 462
QY 357 ERKRSLEYNQDPYRERYEALDEIRNLRIWAGK--RSLRPNQK 400
DB 463 ETKRSLEYNQDKYREKYEKQMDIRDLEIWRAGKAVRSILRPNQK 508
RESULT 5
Q5BAA4 EMENI PRELIMINARY; PRT; 400 AA.
AC Q5BAA4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=AN2526.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Arrhen B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collimore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
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RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor T., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AACD01000043; EAA64631.1; -; Genomic DNA.
DR GO: GO:0004455; F.ketol-acid reductoisomerase activity; IEA.
DR GO: GO:0016491; F.oxidoreductase activity; IEA.
DR GO: GO:0009082; P.branched chain family amino acid biosynthesis; IEA.
DR InterPro: IPR005056; ACh_isomrdctse.
DR Pfam: PF01450; ILVC; 1.
DR TIGRFAMs: TIGR00465; ilvc; 1.
KW Hypothetical protein.
SQ SEQUENCE 400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
Query Match 77.2%; Score 1611; DB 2; Length 400;
Best Local Similarity 78.1%; Pred. No. 8.6e-106;
Matches 314; Conservative 36; Mismatches 48; Indels 4; Gaps 3;
QY 1 MAARNCTKALRPLARQLATPAVQRFTFAAASAVASVAVKAVAPARQVRGVKTMDFA 60
DB 1 MASRGLPRALR-VAARVAPRSVSAALPRPSLAKIAANAVPRVAPV-VPVRGVKTISFA 58
QY 61 GHKEEVRADWPAEKLDDYFKNDTLALIGYSGQHGQGLNLDNGLNVIIVGRKNGKSW 120
DB 59 DSQETVIERADWPKEKLQYFKNDTLALIGYSGQHGQGLNLDQGLNVIIVGRKDGASW 118
QY 121 EDIAIDGWVPGKKNLFDVDEAISRGITVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
DB 119 KEAIDGWVPGKKNLFEVTEAVQKGTITVMNLLSDAAQSETWPTLKPIITKGKTLYFSHGFS 178
QY 181 PVFKDLTKVEVPTDNDVILVAPKSGRTVRSILFRGGRGINSFAVYQDVTGKAKEKAVAL 240
DB 179 PVFKELTKVDVPSDNDVILVAPKSGRTVRTLFRGGRGINSIAVYQDVTGKAKEKAIAM 238
QY 241 GVAVSGYLTYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 300
DB 239 GVAVSGYLTYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
QY 301 EATQSLYPLIGAHGMDWDFDACSITARRGAIDWTPKFKDALKPVFNLLYDSVKNGDERKR 360
DB 299 EATQSLYPLIGANGDMWYAACTTARRGAIDWSRFRKDNKLPFNELYDSVRDGTETQR 358
QY 361 SLEYNQDPYRERYEALDEIRNLRIWAGK--RSLRPNQK 400
DB 359 SLDYNSQDKYREKYEKQMDIRDLEIWRAGKAVRSILRPNQK 400
RESULT 6
Q6CAF8 YARLI PRELIMINARY; PRT; 398 AA.
AC Q6CAF8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome D of strain ClIB99 of Yarrowia
DE lipolytica.
GN OrderedLocusNames=YALI0D03135g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIB 122 / E 150;
```


OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000112; EAK94923.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE 400 AA; 44848 MW; ACD3162D05078D81 CRC64;

Query Match 73.8%; Score 1539.5; DB 2; Length 400;
Best Local Similarity 73.1%; Pred. No. 1e-100;
Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;
QY 1 MAARNCTKALRPLARQLATPAVORRTFVAASA-----VRASVAVKAAVAPARQOVRGKVT 56
DB 1 MSFRITSMRWARLATAKAT--LSKRTFSLANATTRYTAASAAMKAMTPT--SIRGVKT 56
QY 57 MDFAGKEEVHERADWPAEKLLDYFNKDTLALIGYSGQGGQGLNLDNGLNVIVGRKN 116
DB 57 INFGTTEVVERADWPAEKLLDYFNKDTLALIGYSGQGGQGLNLDNGLNVIVGRK- 115
QY 117 GKSWDAIQDQWVPGKLVFDVDEAISRGTIVNNLLSDAAQSTWPHIKPQITKGKTLYS 176
DB 116 GSSWEAAVEDGWPGENLFEVDIAAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAEK 235
QY 237 AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFN 296
DB 236 AIAMATAIGSGYVYKTTTFRVNSDLYGERGCLMGHGMFLAQYEVLRENGHTPSEAFN 295
QY 297 ETVEEATQSLYPLIGAGHDMDFDACSITARRGAIDWTPKFDALKPVFNNDYSVKNGD 356
DB 296 ETVEEATQSLYPLIGKGYMDYDACSITARRGALDWYPRFKDALKPVFEELYESVKNGS 355
QY 357 ERKRSLEYNSQDPRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
DB 356 ETKRSLEFNSDSYDKERLEELQTIIRNMEIWRVKGKVRKLRPENQ 400

RESULT 9
Q59XR8 CANAL PRELIMINARY; PRT; 400 AA.
AC Q59XR8;
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Likely mitochondrial ketol-acid reductoisomerase.
GN Name=ILV5; ORFName=Cao19.88;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000106; EAK95225.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE 400 AA; 44882 MW; FC79162D05078D8C CRC64;

Query Match 73.6%; Score 1535.5; DB 2; Length 400;
Best Local Similarity 72.8%; Pred. No. 1.9e-100;
Matches 295; Conservative 47; Mismatches 52; Indels 11; Gaps 5;
QY 1 MAARNCTKALRPLARQLATPAVORRTFVAASA-----VRASVAVKAAVAPARQOVRGKVT 56
DB 1 MSFRITSMRWARLATAKAT--LSKRTFSLANATTRYTAASAAMKAMTPT--SIRGVKT 56
QY 57 MDFAGKEEVHERADWPAEKLLDYFNKDTLALIGYSGQGGQGLNLDNGLNVIVGRKN 116
DB 57 INFGTTEVVERADWPAEKLLDYFNKDTLALIGYSGQGGQGLNLDNGLNVIVGRK- 115
QY 117 GKSWDAIQDQWVPGKLVFDVDEAISRGTIVNNLLSDAAQSTWPHIKPQITKGKTLYS 176
DB 116 GSSWEAAVEDGWPGENLFEVDIAAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAEK 235
QY 177 HGFSVPFKDLTKVEPTDVTDLVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAEK 236
DB 176 HGFSVPFKDLTKVEPTDVTDLVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAEK 235
QY 237 AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFN 296
DB 236 AIAMATAIGSGYVYKTTTFRVNSDLYGERGCLMGHGMFLAQYEVLRENGHTPSEAFN 295
QY 297 ETVEEATQSLYPLIGAGHDMDFDACSITARRGAIDWTPKFDALKPVFNNDYSVKNGD 356
DB 296 ETVEEATQSLYPLIGKGYMDYDACSITARRGALDWYPRFKDALKPVFEELYESVKNGS 355
QY 357 ERKRSLEYNSQDPRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
DB 356 ETKRSLEFNSDSYDKERLEELQTIIRNMEIWRVKGKVRKLRPENQ 400

RESULT 10
Q6CV71 KLULA PRELIMINARY; PRT; 397 AA.
AC Q6CV71;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-1140 of Kluyveromyces lactis.
GN OrderedLocusNames=KLIA0A02673g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI_TaxID=28985;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
 RX PubMed=15292952; DOI=10.1038/nature02579;
 RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,
 RA Goffard N., Franchou L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boiarane A., Boyer J., Catilicco L., Confalonieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hancraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.-M., Nikolski M., Ozcas G.-P., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudon R., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR382121; CAH02706.1; -- Genomic DNA.
 DR GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR00506; ACH_isomrctase.
 DR Pfam; PF01450; IlvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 KW Complete proteome.
 SQ SEQUENCE 397 AA; 44189 MW; 7634BEC037ABAA9B CRC64;
 Query Match 73.1%; Score 1524; DB 2; Length 397;
 Best Local Similarity 74.6%; Pred. No. 1.2e-99;
 Matches 294; Conservative 37; Mismatches 57; Indels 6; Gaps 2;
 QY 11 RPLARQLATPA----VQRRTFVAASAVRASVAVKAAAPAAQVRGKVTMDFAHKEEV 66
 DB 3 RQAARQLIANSRVTAKRAISFAARQSTVSLRSTAFASKEPLVATRGKIQNFGVSETV 62
 QY 67 HERADWPAKLLDYFKNDTLALIGYSGHGGHGLNLDNGNLNVTGVKNGKSWEDIAQD 126
 DB 63 YERADWPEKLLQYFKDDTLALIGYSGYGGYGGGLNLDNGNLNVTGVKNGASWKAIED 122
 QY 127 GWVPGKGLFVDEAISRGTVVNLISDAQSETWPHIKPQITKTKTLYFSGHSPVPFKDL 186
 DB 123 GWVPGKGLFVDEAVQKTVVNLISDAQSETWSSLUKPLTKTKTLYFSGHSPVPFKDL 182
 QY 187 TKVBPVTDVILVAPKSGRTVRSFLREGKINSFVAVQDVTGKAKAKAVALGVAAGS 246
 DB 183 THVEPPTDIDILVAPKSGRTVRSFLKEGRGINSFVAVNDVTGKAHKAQALAVAGS 242
 QY 247 GYLVTTFEKEVYSDLYGERGCLGGHGMFLAQYEVILRERHSPSFAFNETVEATQSL 306
 DB 243 GYVYQTTFEKEVNSDLYGERGCLGGHGMFLAQYEVILRERHSPSFAFNETVEATQSL 302
 QY 307 YPLIGAHGDMWPDACSTARRGALDTPKFKDALKPVFNLYDSVKNRKRSLFVNS 366
 DB 303 YPLIGKGMIDWPDACSTARRGALDTPKFKDALKPVFNLYDSVKNRKRSLFVNS 362
 QY 367 QPDYRERYAELEIRNLWEIRWAGK--RSLRPN 398
 DB 363 QPDYREREAELEIRNLWEIRWAGK--RSLRPN 396
 RESULT 11
 ID ILV5 YEAST
 AC P06168; STANDARD; PRT; 395 AA.
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, last sequence update)
 DT 13-SEP-2005 (Rel. 48, last annotation update)
 DE ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
 DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
 DE reductoisomerase).
 GN Name=ILV5; OrderedLocusNames=YLR355C; ORFNames=L9638.7;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87117524; PubMed=3027658;
 RX Petersen J.G.L., Holmberg S.;
 RT "The ILV5 gene of Saccharomyces cerevisiae is highly expressed.";
 RL Nucleic Acids Res. 14:9631-9651(1986).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,
 RA Ansong W., Bense V., Brueckner M., Delius H., Dubois E.,
 RA Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U.,
 RA Heumert P., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K.,
 RA Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E.,
 RA Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M.,
 RA Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C.,
 RA Schwarz S., Underwood A.P., Urrastarazu L.A., Vandenbol M.,
 RA Verhaaselt P., Vierendeels F., Voet M., Volckaert G., Voss H.,
 RA Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
 RA Hani J., Hoheisel J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 [3]
 RN PROTEIN SEQUENCE OF 166-174.
 RP STRAIN=S288C;
 RC MEDLINE=95203288; PubMed=7895733;
 RX Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R.; McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 database.";
 RL Electrophoresis 15:1466-1486(1994).
 [4]
 RN IDENTIFICATION OF PROBABLE N-TERMINUS.
 RP MEDLINE=97121404; PubMed=8962070; DOI=10.1073/pnas.93.25.14440;
 RX Shevchenko A., Jensen O.N., Podtelejnikov A.V., Sagliocco F., Wilm M.,
 RA Varm O., Mortensen P., Shevchenko A., Boucherie H., Mann M.;
 RT "Linking genome and proteome by mass spectrometry: large-scale
 identification of yeast proteins from two dimensional gels.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445(1996).
 CC -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
 CC -1- Isoleucine from 2-oxobutanoate; step 2.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
 CC from pyruvate; step 2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X04969; CAA28643.1; -- Genomic DNA.
 CC EMBL; U19102; AAB67753.1; -- Genomic DNA.
 CC FIR; A24709; A24709.
 CC HSP; Q01292; IOMG.
 CC IntAct; P06168; --
 CC GeneOnline; 142419; --
 CC SWISS-2DPAGE; P06168; YEAST.
 CC Ensembl; YLR355C; Saccharomyces cerevisiae.
 CC SGD; S000004347; ILV5.
 CC GO; GO:0042645; C:mitochondrial nucleoid; IDA.

DR	GO; GO:0005739; C:mitochondrion; IDA.
DR	GO; GO:0004455; P:ketoacid reductoisomerase activity; TAS.
DR	GO; GO:0009082; P:branched-chain family amino acid biosynthesis; TAS.
DR	GO; GO:0000002; P:mitochondrial genome maintenance; IMP.
DR	InterPro; IPR000506; ACh_isomrdctae.
DR	Pfam; PF01450; IlvC; 1.
DR	TIGRFAMs; TIGR00465; ilvC; 1.
KW	Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
KW	Complete proteome; Direct protein sequencing; Magnesium;
KW	Mitochondrion; NADP; Oxidoreductase; Transit peptide.
FT	TRANSIT 1 47 Mitochondrion (Potential).
FT	CHAIN 48 395 Ketol-acid reductoisomerase.
FT	N_BIND 84 93 NADP (Potential).
FT	REGION 363 395 Hydrophilic.
FT	ACT SITE 171 171 Potential.
SQ	SEQUENCE 395 AA; 44368 MW; D76419A6AD68E85E CRC64;

Query Match		72.3%;	Score 1508.5;	DB 1;	Length 395;
Best Local Similarity		73.6%;	Pred. No. 1.6e-98;		
Matches 295;		Conservative 39;	Mismatches 50;	Indels 17;	Gaps 5;

Qy	7	TKALRPRLARQLATPAVORRTTVAASAVRASVAKAVAAPARQQV-----RGVKTMDFPA	60
Db	4	TOAARLICNSRVITA--KRTP---ALATRAA----AYSRPAARFVKPMITTGLKQINFG	54
Qy	61	GHKEEVHERADWPAEKLIDYFKNDTLALIGYSOGHGQGLNLRDNLNVIIVGRKNGKSW	120
Db	55	GTVETVVERADWPREKLIDYFKNDTFALLIGYSOGYGQGLNLRDNLNVIIVGRKDGSW	114
Qy	121	EDATODGVPGKNLFDVDEAISRGTVIYNLLSDAAQSSTWPHIKPIQTGKTLYFSHGFS	180
Db	115	KAAYIEDGWPGKNLFTVEDAIKRGSYVMNLLSDDAQSETWPAIKPLLTKGTYLSHGFS	174
Qy	181	PVFKDLTKVEVPTDVDILVAPKGSGRTVRSLPREGRGINSFPAYQDVTKAKEKVAL	240
Db	175	PVFKDLTHVESPPKOLDVILVAPKGSGRTVRSLFKEGRGINSYAVMNDVTGKAHEKAQAL	234
Qy	241	GVAVSGYLVEYTEPEKYVDLYGBERGCLMGCIHGMFLAQYEVLRRERGHSPSEAFNETVE	300
Db	235	AVAIGSGVVGYTTFEREVNSDLYGBERGCLMGCIHGMFLAQVDVURENGHSSEAFNETVE	294
Qy	301	EATOSLYPLIGHAGMDWMFDCASTTARRGAIDWTPKFKDALPKVPFNMLYDSVXNGDKRK	360
Db	295	EATOSLYPLIGKYDMYMYDACSTTARRGALDWYPFKNALKPVPQDIYSTKNGTETR	354
Qy	361	SLEVNSQDPYRERYEAELDEIRNLEIWPAKG--RSLRPENQ	399
Db	355	SLEFNSQDPYREKLEKELDITRNMEIWKVGKEVRKLRPENQ	395

RESULT 12

ID	Q02341_YEAST PRELIMINARY;	PRT;	395 AA.
AC	Q02341;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Acetohydroxy-acid isomeroeductase.		
GN	Name=IlvS; Synonyms=ILV5X;		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OX	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
NCBI_TaxID=4932;			
RN	[1]		
RP	Nucleotide SEQUENCE.		
RX	MEDLINE=9519792; PubMed=7874731; DOI=10.1007/BF000309925;		
RA	Xie Q., Jimenez A.;		
RT	"Cloning and molecular analysis of two different ILV5 genes from a		
RT	brewing strain of Saccharomyces cerevisiae.";		
RL	Curr. Genet. 26:3398-402(1994).		
REMBL; S77496;			
HSSP; Q01292; IQMG.			
DR	Ensembl; YLR355C; Saccharomyces cerevisiae.		

RL	Nature 430:35-44 (2004).	
DR	EMBL; CR380948; CAG58005.1; --; Genomic_DNA.	
DR	GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.	
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.	
DR	GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.	
DR	InterPro; IPR000506; ACh_isomrctase.	
DR	Pfam; PF01450; ilvC; 1.	
DR	TIGRFAMs; TIGR00465; ilvC; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 399 AA; 44568 MW; E2241C86A034D728 CRC64;	
Query Match		
Best Local Similarity 74.1%; Score 1500.5; DB 2; Length 399;		
Matches 286; Conservative 40; Mismatches 45; Indels 15; Gaps 3;		
Qy	24 RRTFAAASA-----VRASVAVKAAVAPARQQVRGKTMDFAGHKEEYHERADWPAE 75	
Db	19 KRTFAAARAASMPRAASLMAQSIKPIVA-----TRGIKQINFGGTVETVYERADPRE 73	
Qy	76 KLIDYFNKDITALLIGYSGHGGQGLNRDNGLVIVGRKNGKSWEDAIQDGVGPKQLF 135	
Db	74 KLLNFANDTPTALLIGYSGYGGQGLNRDNGLVIIIGVRKDGASWKAIEDGWYFGENLF 133	
Qy	136 DVDEAIGRTVWMLLSDAAQSETPHLPKPTITKGTLYFSHGSPFVKDLTKVEVPTDV 195	
Db	134 EVEAVKGTVMWMLLSDAAQSETPHLPKPTITKGTLYFSHGSPFVKDLTKVEVPTDV 193	
Qy	196 DVLIVAPKSGRTVRSIFREGGINSSFAVYQDVTGKAKAVAGVAVSGVLYETTFE 255	
Db	194 DVLIVAPKSGRTVRSIFKEGGINSSFAVWVNDVSGKAHEKAQALAVAGVGYVYQITFE 253	
Qy	256 KEVYSDLYGERGCLMGHIGHFLAQYEVLRERHSPSEAFNETVEEATQSLYPLIGAHGM 315	
Db	254 KEVNSDLYGERGCLMGHIGHFLAQYEVLRERHSPSEAFNETVEEATQSLYPLIGYGM 313	
Qy	316 DMWEDACSTARRCAIDWTPKFDALPVENNLVDSVKNRDKRSLEYSNQPDYREYE 375	
Db	314 DYMIDACSTARRGALDWPYIFKDALPVPFDLYESTNGSETKRSLEFNSQPDYREKLE 373	
Qy	376 AELDEIRNLEIWRAGK--RSLRPNQ 399	
Db	374 SELQTIRMEIWRVGVKEVRLRPNQ 399	
RESULT 14		
ILV5 SCHPO	STANDARD; PRT; 404 AA.	
ID	P78827; 042619;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	13-SEP-2005 (Rel. 48, Last annotation update)	
DE	Probable ketol-acid reductoisomerase, mitochondrial precursor	
DE	(EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase)	
GN	Name=ilv5; ORFNames=SPBC56F2.12;	
OS	Schizosaccharomyces pombe (Fission yeast).	
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;	
OC	Schizosaccharomycetes.	
OX	NCBI_TaxID=4896;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=972;	
RC	MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;	
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,	
RA	Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,	
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,	
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,	
RA	Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,	
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,	
RA	James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,	
RA	Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,	
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,	
RA	Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,	
RA	Skellton J., Simmonds M.N., Squares R., Squares S., Stevens K.,	
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,	
RA	Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,	
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,	
RA	Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,	
RA	Hilbert H., Borzym K., Langer I., Beck A., Lehman H., Reinhardt R.,	
RA	Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Fumelle B.,	
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,	
RA	Gallier F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,	
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	
RA	Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,	
RA	Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;	
RT	"The genome sequence of Schizosaccharomyces pombe.";	
RL	Nature 415:871-880 (2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RC	STRAIN=PR745;	
RC	MEDLINE=98162722; PubMed=9501991;	
RX	Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;	
RA	"Identification of open reading frames in Schizosaccharomyces pombe	
RT	cDNAs.";	
RL	DNA Res. 4:363-369 (1997).	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE OF 262-404.	
RA	Kawamukai M.;	
RA	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.	
CC	-1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.	
CC	-1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.	
CC	-1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.	
CC	-1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.	
CC	-1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).	
CC	-1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
CC	EMBL; AL023288; CAA18891.1; --; Genomic_DNA.	
DR	EMBL; D89175; BAA13837.1; --; mRNA.	
DR	EMBL; AB009603; BAA24000.1; --; mRNA.	
DR	PIR; T40532; T40532.	
DR	HSSP; Q9HVA2; INP3.	
DR	GeneDB Spombe; SPBC56F2.12; --.	
DR	InterPro; IPR000506; ACh_isomrctase.	
DR	Pfam; PF01450; ilvC; 1.	
DR	TIGRFAMs; TIGR00465; ilvC; 1.	
KW	Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;	
KW	Complete proteome; Mitochondrion; NADP; Oxidoreductase;	
KW	Transit peptide.	
FT	TRANSIT 1 ? Mitochondrion (Potential).	
FT	CHAIN 1 ? Probable ketol-acid reductoisomerase.	
FT	ACT_SITE 178 178 Potential.	
FT	CONFLICT 38 38 S -> R (in Ref. 2).	
FT	CONFLICT 92 92 Y -> S (in Ref. 2).	
FT	CONFLICT 275 275 N -> P (in Ref. 2).	
FT	CONFLICT 297 297 N -> P (in Ref. 2).	
FT	CONFLICT 394 394 V -> G (in Ref. 2).	
SQ	SEQUENCE 404 AA; 45189 MW; 9AB3674C71AD6FEB CRC64;	
Query Match		
Best Local Similarity 69.7%; Score 1494.5; DB 1; Length 404;		
Matches 287; Conservative 52; Mismatches 46; Indels 27; Gaps 4;		
Qy	2 AARNCTKALRPL-ARQLATPAVQRRFTFAAASAVRASVAVKAVAPARQ-----Q 50	

Db	6	SSRMANKALRTMGSRRLATRSM-----SVWARTTAAPSMRFPAPRTAPLMQ	51
Qy	51	VRGVKTMDFAGHKEEVEHERADWPAEKLLDYFKNDTTLALIGYSGQGHGQGLNRDGLNVI	110
Db	52	TRGMRVMDFAGTKENWNERSDWPREKLVDPKNDTTLAIIIGYSGQGHGQGLNARDQGLNVI	111
Qy	111	VGVKNGKSWEDAIQDGWPGKNLFDVDEAISRTTIWMNLLSDAAQSETWPHIKPOITKG	170
Db	112	VGVKDGASWKQAIEDGWPGKTLFPVEEAIKGSIIIMNLLSDAAQSETWPKIAPLITKG	171
Qy	171	KTLYFSHGFSVPFKDLTKVEYPTDVIDVILVAPKSGSRTVRSLPREGRGINSFVAVQDVT	230
Db	172	KTLYFSHGFSVIFKQDKIHPPKXDVILVAPKSGSRTVRTLFPKEGRGINSFVAVQDVT	231
Qy	231	GKAKEKAVAGVAVGSGYL YETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGH	290
Db	232	GKAQEKAIGLAVAVGSGFIYQTTFKKEVISDLVGERGCLMGGINGLFLAQYQVLRERGH	291
Qy	291	PSEAFNETVEEATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPFKDALKPVFNLYD	350
Db	292	PAEAFNETVEEATQSLYPLIGKYGLDYMFACSTTARRGAIDWTPRPLEANKKVLNELYD	351
Qy	351	SVKNGDERKRSLEYNQSDYRERYEAELDEIRNLEIWRAGK--RSLRPNQK	400
Db	352	NVNGENAKRSLEYNSAPNYRELYDKLEELIRNLEIWKAGEVVRSLRPEHNK	403
RESULT 15			
Q02340 YEAST			
ID	Q02340	YEAST PRELIMINARY; PRT; 395 AA.	
AC	Q02340;		
DT	01-NOV-1996	(TrEMBLrel. 01, Created)	
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Acetohydroxy-acid isomeroreductase.		
GN	Name=ILV5G;		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
OX	NCBI_TaxID=4932;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;		
RA	Xie Q., Jimenez A.;		
RT	"Cloning and molecular analysis of two different ILV5 genes from a		
RT	brewing strain of Saccharomyces cerevisiae.";		
RL	Curr. Genet. 26:398-402(1994).		
DR	EMBL; S77495; AAB33578.1; -; Genomic_DNA.		
DR	HSSP; Q01292; 1QMG.		
DR	Ensembl; YLR355C; Saccharomyces cerevisiae.		
DR	GO; GO:0004455; F:keto1-acid reductoisomerase activity; IEA.		
DR	GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.		
DR	InterPro; IPR000506; ACh_isomrdctse.		
DR	Pfam; PF01450; IlvC; 1.		
DR	TIGRFAMs; TIGR00465; ilvC; 1.		
SQ	SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2AEF CRC64;		
Query Match			
Best Local Similarity 70.9%; Score 1479.5; DB 2; Length 395;			
Matches 288; Conservative 43; Mismatches 55; Indels 13; Gaps 4;			
Qy	7	TKALRPLARQLATPAVQRTEV----AAASAVRASVAVKAVAPARQQVRGVKTMDFAGH	62
Db	4	TOAARLICNSRVVTA--KRTFALATRAAAYSRPAARFVKFWA-----TRGLKQINFGGT	56
Qy	63	KEEVHERADWPAEKLLDYFKNDTTLALIGYSGQGHGQGLNRDGLNVI VGVKNGKSWED	122
Db	57	VETVYERADWPREKLLNLYFKDDTFLALIGYSGQGYGQGLNRDGLNVIIGVRKDGASWKA	116
Qy	123	AIDQGWPGKNLFDVDEAISGTVNMNLLSDAAQSETWPHIKPOITKGKTLFSGHGFSPV	182
Db	117	AIEDGWVPGQNLFSVEDAIKGNVNMNLLSDAAQSETWPTIKPLLTGKTLFSGHGFSPV	176
Qy	183	FKDLTKVEYPTDVIDVILVAPKSGSRTVRSLPREGRGINSFVAVQDVTGKAKEKAVAGV	242
Db	177	FKDLTHVEPPKDLVDILVAPKSGSRTVRSLPKEGRGINSFYAVMNDVTGKAHEKAQALAV	236
Qy	243	AVGSGYL YETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA	302
Db	237	AIGSGYVYQTTFFEREVNSDLVGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEA	296
Qy	303	TQSLYPLIGAHGMDWMDACSTTARRGAIDWTPFKDALKPVFNLYDSVKNGDERKRS	362
Db	297	TQSLYPLIGKYGMDYMDACSTTARRGALDWPIPKNALPVPFQDLYESTKNGTETKRS	356
Qy	363	EYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPNQ	399
Db	357	EFNSQPDYREKLEKELVTIRNMEIWKVGEVVKLRPENK	395
Search completed: March 22, 2006, 15:33:26			
Job time : 126.313 secs			

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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 114.954 Seconds
(without alignments)
1528.885 Million cell updates/sec

Title: US-10-797-248A-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRKRSILRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	400	6	ABR64305
2	1860	89.2	400	6	ABR64306
3	1860	89.2	400	9	ADV16807
4	1856	89.0	402	6	ABR64303
5	1658	79.5	403	9	ADV16810
6	1633	78.3	396	6	ABJ26477
7	1633	78.3	508	6	ABJ26502
8	1604	76.9	388	6	ABJ25902
9	1604	76.9	500	6	ABJ25877
10	1539.5	73.8	400	4	AAU15089
11	1539.5	73.8	400	5	ABP73238
12	1508.5	72.3	395	6	ABR64304
13	1508.5	72.3	395	7	ADK64188
14	1423.5	68.2	409	7	ADB70124
15	1084.5	52.0	347	6	ABU20976
16	486	23.3	332	4	ABR6356
17	486	23.3	586	2	AAJ26182
18	483	23.2	342	4	AAU01250
19	480.5	23.0	331	5	ABR48168
20	480.5	23.0	331	6	ABU32456
21	473	22.7	579	2	AAJ26183
22	473	22.7	579	2	AAJ26180
23	473	22.7	585	8	ADK93651
24	473	22.7	585	8	ADX88429

25	473	22.7	588	8	ADY07198
26	473	22.7	590	8	ADY07344
27	473	22.7	590	8	ADY07344
28	472.5	22.7	326	7	ADM36226
29	472.5	22.6	579	3	AAG35210
30	472	22.6	596	3	AAG35209
31	467	22.4	581	9	ADY61069
32	465	22.3	549	3	AAG26356
33	465	22.3	591	5	ABB92723
34	465	22.3	591	8	ADT55519
35	463	22.2	337	6	ABU24174
36	463	22.2	571	8	ADY04361
37	462	22.1	568	8	ADY07450
38	462	22.1	578	8	ADY07435
39	462	22.1	626	8	ADY07435
40	461.5	22.1	334	4	AAG81458
41	461.5	22.1	334	6	ABU42920
42	461.5	22.1	339	5	ABP39068
43	461.5	22.1	339	8	ADU07053
44	454.5	21.8	336	6	ABU18526
45	453.5	21.7	482	3	AAG26357

ALIGNMENTS

RESULT 1
ABR64305
ID ABR64305 standard; protein; 400 AA.
XX
AC ABR64305;
XX

DT 16-SEP-2003 (first entry)
XX

DE Acetohydroxyacid isomeroreductase.
XX

KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX

OS Neurospora crassa.
XX

PN FR2829363-A1.
XX

PD 14-MAR-2003.
XX

PF 10-SEP-2001; 2001PR-00011689.
XX

PR 10-SEP-2001; 2001PR-00011689.
XX

PA (AVET) AVENTIS CROPS SCIENCE SA.
XX

PI Dumas R; Lebrun MH, Zundel JL, Effantin G, Morin V;
XX

DR WPI; 2003-405775/39.
XX

PT Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase.
XX

PS Claim 2; Fig 1; 66pp; French.
XX

CC The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
XX

SQ Sequence 400 AA;
XX

Query Match 100.0%; Score 2086; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1e-191;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
 DB 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
 QY 61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYSGQGHGQGLNLDNGLNVIIVGRKNGKSW 120
 DB 61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYSGQGHGQGLNLDNGLNVIIVGRKNGKSW 120
 QY 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
 DB 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
 QY 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
 DB 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
 QY 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
 DB 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
 QY 301 EATQSLYPLIGAHGMDWMPDACSITARRGAIDWTPKFDALKPFVFNLYDSVKNGDERK 360
 DB 301 EATQSLYPLIGAHGMDWMPDACSITARRGAIDWTPKFDALKPFVFNLYDSVKNGDERK 360
 QY 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGKRSRLENQK 400
 DB 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGKRSRLENQK 400

RESULT 2
 ABR64306
 ID ABR64306 standard; protein; 400 AA.
 XX
 AC ABR64306;
 XX

DT 16-SEP-2003 (first entry)
 XX
 DE Acetohydroxyacid isomeroreductas #2.
 XX
 KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
 XX
 OS Magnaporthe grisea.
 XX
 PN FR2829363-A1.
 XX
 PD 14-MAR-2003.
 XX
 PF 10-SEP-2001; 2001FR-00011689.
 XX
 PR 10-SEP-2001; 2001FR-00011689.
 XX
 PA (AVET) AVENTIS CROPS SCIENCE SA.
 XX

PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX
 DR WPI; 2003-405775/39.
 XX
 DR N-PSDB; ACC80185, ACC80186.
 XX
 PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
 PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroreductase.
 XX
 PS Disclosure; Page 57-58; 66pp; French.
 XX

CC The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (I) of acetohydroxyacid
 CC isomeroreductase. (II) are used for curative or preventative treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
 CC to illustrate the invention
 XX
 SQ Sequence 400 AA;

Query Match 89.2%; Score 1860; DB 6; Length 400;
 Best Local Similarity 87.1%; Pred. No. 1.2e-169;
 Matches 350; Conservative 34; Mismatches 14; Indels 4; Gaps 2;
 QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
 DB 1 MSARGFSKALRPMARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 58
 QY 61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYSGQGHGQGLNLDNGLNVIIVGRKNGKSW 120
 DB 59 GHKEEVHERADWPAEKLLDYFKNDTLALIGYSGQGHGQGLNLDNGLNVIIVGRKNGKSW 118
 QY 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
 DB 119 KDAVQDQWPGKGLFEVDEAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 178
 QY 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
 DB 179 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 238
 QY 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
 DB 239 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 298
 QY 301 EATQSLYPLIGAHGMDWMPDACSITARRGAIDWTPKFDALKPFVFNLYDSVKNGDERK 360
 DB 299 EATQSLYPLIGAHGMDWMPDACSITARRGAIDWTPKFDALKPFVFNLYDSVKNGSETQR 358
 QY 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGK--RSRLENQK 400
 DB 359 SLDYNSQPDYREKYEAEEMEIRNLEIWRAGKAVRSRLENQK 400
 RESULT 3
 ADVI6807
 ID ADVI6807 standard; protein; 400 AA.
 XX
 AC ADVI6807;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE M grisea ketol-acid reductoisomerase ILV5 seqid 6.
 XX
 KW substrate inhibition; antibiotic; gene disruption;
 KW ketol-acid reductoisomerase; ILV5, enzyme.
 XX
 OS Magnaporthe grisea.
 XX
 PN WO2004104176-A2.
 XX
 PD 02-DEC-2004.
 XX
 PF 17-MAY-2004; 2004WO-US015404.
 XX
 PR 15-MAY-2003; 2003US-0470947P.
 PR 19-MAY-2003; 2003US-0471615P.
 PR 21-MAY-2003; 2003US-0472242P.
 XX
 PA (PARA-) PARADIGM GENETICS INC.
 XX
 PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
 PI Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger RW;
 PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX
 DR WPI; 2005-021202/02.
 DR N-PSDB; ADVI6805, ADVI6806.
 XX
 PT Identifying a test compound as a candidate for an antibiotic comprises
 PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
 PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
 PT with a test compound.
 XX
 PS Claim 48; SEQ ID NO 6; 179pp; English.

XX The invention describes a method of identifying a test compound as a
CC candidate for an antibiotic comprising contacting ornithine
CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
CC or fungal pathogenicity-conferring gene with a test compound. The method
CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
CC ; and detecting the presence or absence of binding between the test
CC compound and the polypeptide or gene, where binding indicates that the
CC test compound is a candidate for an antibiotic. Also described are: an
CC isolated nucleic acid comprising a nucleotide sequence encoding a
CC polypeptide having at least 50% sequence identity to, or having at least
CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
CC polypeptide consisting essentially of the amino acid sequence of 400, 403
CC or 469 amino acids. The methods are useful for identifying inhibitors of
CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
CC pathogenicity-conferring gene as antibiotics. This is the amino acid
CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
XX
SQ Sequence 400 AA;

Query Match 89.2%; Score 1860; DB 9; Length 400;
Best Local Similarity 87.1%; Pred. No. 1.2e-169;
Matches 350; Conservative 34; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MAARNCTKALRPLARQLATPAVQRRTFAAASAVRASVAVKAAVAPARQVGVKTMDF 60
Db 1 MSARGFSKALRPMARQLATPAVQRRTFAAASVVRAT--RKAAPVPTQQQIRGVKTMDF 58
Qy 61 GHKEEVEHERADWPAEKLLDYFKNDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 120
Db 59 GHKEQWVERADWPKEKLELYFKDDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 118
Qy 121 EDATQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 180
Db 119 KDAVQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 178
Qy 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLSFREGGINSSFAVYQDVTGKAKEKAV 240
Db 179 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLSFREGGINSSFAVYQDVTGKAKEKAV 238
Qy 241 GVAVGSGLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 300
Db 239 GVAIGSGLYKTTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 298
Qy 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBDKR 360
Db 299 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBDKR 358
Qy 361 SLEYNQSDPYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
Db 359 SLDYNSQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400

RESULT 4
ABR64303
ID ABR64303 standard; protein; 402 AA.
XX
AC ABR64303;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductase #1.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Magnaporthe grisea.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.

XX 10-SEP-2001; 2001FR-00011689.
PR (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX
XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
XX Claim 2; Fig 1; 66pp; French.
XX
XX The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase (II) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 402 AA;

Query Match 89.0%; Score 1856; DB 6; Length 402;
Best Local Similarity 86.8%; Pred. No. 2.8e-169;
Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MAARNCTKALRPLARQLATPAVQRRTFAAASAVRASVAVKAAVAPARQVGVKTMDF 60
Db 1 MSARGFSKALRPMARQLATPAVQRRTFAAASVVRAT--RKAAPVPTQQQIRGVKTMDF 58
Qy 61 GHKEEVEHERADWPAEKLLDYFKNDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 120
Db 59 GHKEQWVERADWPKEKLELYFKDDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 118
Qy 121 EDATQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 180
Db 119 KDAVQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 178
Qy 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLSFREGGINSSFAVYQDVTGKAKEKAV 240
Db 179 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLSFREGGINSSFAVYQDVTGKAKEKAV 238
Qy 241 GVAVGSGLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 300
Db 239 GVAIGSGLYKTTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 298
Qy 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBDKR 360
Db 299 EATQSLYPLIGAHGMDWMDACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBDKR 358
Qy 361 SLEYNQSDPYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
Db 359 SLDYNSQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400

RESULT 5
ADV16810
ID ADV16810 standard; protein; 403 AA.
XX
AC ADV16810;
XX
DT 24-FEB-2005 (first entry)
XX
DE M graminicola ketol-acid reductoisomerase KAR1 seqid 9.
XX
KW substrate inhibition; antibiotic; gene disruption;
KW ketol-acid reductoisomerase; KAR1; enzyme.
XX
OS Mycosphaerella graminicola.
XX
PN W02004104176-A2.

XX PD 02-DEC-2004.

XX PF 17-MAY-2004; 2004WO-US015404.

XX PR 15-MAY-2003; 2003US-0470947P.

XX PR 19-MAY-2003; 2003US-0471615P.

XX PR 21-MAY-2003; 2003US-0472242P.

XX PA (PARA-) PARADIGM GENETICS INC.

XX PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC, Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW, Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR; WPI; 2005-021202/02.

XX DR N-PSDB; ADV16802, ADV16808, ADV16809.

XX PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound.

XX PS Claim 50; SEQ ID NO 9; 179pp; English.

XX CC The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound. The method comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound ; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the test compound is a candidate for an antibiotic. Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a: an polypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids; and an isolated polypeptide consisting essentially of the amino acid sequence of 400, 403 or 469 amino acids. The methods are useful for identifying inhibitors of ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of *Mycosphaerella graminicola* ketol-acid reductoisomerase KARI.

XX SQ Sequence 403 AA;

Query Match 79.5%; Score 1658; DB 9; Length 403;
Best Local Similarity 78.4%; Pred. No. 3.2e-150;
Matches 315; Conservative 40; Mismatches 43; Indels 4; Gaps 2;

QY 1 MAARNCTKALRPLARLATPAVORRTFVAAGAASAVRASV--AVKAAVAPARQVGRVKTWD 58
DB 1 MASKNATRALRASLRQLKAPQVQORSFVAANASRSLVPAQAVTSAFVQVGRGAKTV 60

QY 59 FAGHKEEVHERADWPAAEKLLDYPKNDTLALIGYSGQHGQGLNRDNLNVLVGRKNGK 118
DB 61 FAGDEKVFERDDWPREKLLFYPKNDTLALIGYSGQHGQGLNRDNLNVLVGRKGA 120

QY 119 SHEDATQDCWVGPKNLFDVDEAISRTIWNLLSDAAQSETWPHIKPQTKGTLFSGH 178
DB 121 SWKEAEGDGVGKGNLFDIDTAIGKGTIIMNLLSDAAQSETWPHIKPMLTKGTLFSGH 180

QY 179 FSPVFQDLTKVEPTDVIDVLVAPKSGRTVRSLPREGGINSFSAVYQDVTGKAKEAV 238
DB 181 FSPVFQDLTKVEPTDVIDVLVAPKSGRTVRSLPREGGINSFSAVYQDVTGKAKEAV 240

QY 239 ALGVAVSGYLVTETPEKEVYSDLYGERCLMGHGMFLAQYEVLRERGHSPSEAFNET 298
DB 241 ALGVAVSGVMYKTTPEKEVYSDLYGERCLMGHGMFLAQYEVLRERGHSPSEAFNET 300

QY 299 VEATOSLYPLIGAHGMDWFMFACSTTARRGAIDWTPKFDALKPVFNLLYSVKNGBDR 358
DB 301 VEATOSLYPLIGKNGMDWYMEACSTTARRGAIDWTKRFTKLKPVFEELYDSVTKGT 360

QY 359 KRSLEYNQPDYRERYAELEIRNLEIWRACK--RSLRPEN 398
DB 361 QRTMEYAGKDYREAFKEMEEIRNLEIWRACKAVRSLRPEN 402

RESULT 6
ABJ26477
ID ABJ26477 standard; protein; 396 AA.
XX AC ABJ26477;
XX DT 16-APR-2003 (first entry)
XX DE Aspergillus fumigatus essential gene protein #1135.
XX KW Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection; cancer; contamination; biofilm; antibody; immune response.
XX OS *Aspergillus fumigatus*.
XX PN WO200286090-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013142.
XX PR 23-APR-2001; 2001US-0285697P.
XX PR 27-APR-2001; 2001US-0287066P.
XX PR 05-JUN-2001; 2001US-0295890P.
XX PR 09-JUL-2001; 2001US-0303899P.
XX PR 31-AUG-2001; 2001US-0316362P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM; WPI; 2003-093124/08.
XX DR New purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*, useful for treating or preventing infections by *A. fumigatus*, or for treating a non-infectious disease in a subject e.g. cancer.
XX PT Disclosure; Page; 175pp; English.
XX CC The invention relates to novel purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as *A. fumigatus*, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by *A. fumigatus*, or to prevent or inhibit formation on a surface of a biofilm comprising *A. fumigatus*. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of *A. fumigatus* to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of *Aspergillus fumigatus* of the invention

XX SQ Sequence 396 AA;

Query Match 78.3%; Score 1633; DB 6; Length 396;
 Best Local Similarity 78.6%; Pred. No. 7.9e-148;
 Matches 319; Conservative 35; Mismatches 36; Indels 16; Gaps 6;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAA-----SARVASVAVKAAVAPARQOVRGVKT 56
 DB 1 MASRGLPRALR-LAR-VAAP---RTVISALPRPALAKAATRAASTAP-----VRGVKT 50

QY 57 MDPAGHKEEVEHERADWPAEKLLDYFNKDTLALIGYSGQGHGGLNLDNGNLNIVGVKRN 116
 DB 51 IAFADSKETVYERADWPPEKLEQYFNKDTLALIGYSGQGHGGLNLDNGNLNIVGVKRD 110

QY 117 GKSMEDAIQDGVPGKGLFDVDEALSRGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 176
 DB 111 GASWEAIQDGVPGKGLFDVDEAVQKGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 170

QY 177 HGFSPVFKELTKVVEPTDVIDVILVAPKSGRTVRSIFREGRGINSFAVYQDVVTGKAKEK 236
 DB 171 HGFSPVFKELTKVDVDPKDVILVAPKSGRTVRLFREGRGINSFAVYQDVVTGKAKEK 230

QY 237 AVALGVAVSGSYLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERHSPSEAFN 296
 DB 231 AIAMGVAVSGSYLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERHSPSEAFN 290

QY 297 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWTPKPKDALKPVFNLYDSVKNGD 356
 DB 291 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWSSRFKDTLPKIFNELYDSVRDGT 350

QY 357 ERKRSLEYNQDYPYRYEAELEIRNLEIWRAGKR--SLRPNQK 400
 DB 351 ETKRSLEYNQDYPYRYEAELEIRNLEIWRAGKAVGSLRPNQK 396

RESULT 7
 ID ABJ26502 standard; protein; 508 AA.
 AC ABJ26502;
 XX
 XX
 DT 16-APR-2003 (first entry)
 XX
 XX Aspergillus fumigatus essential gene protein #1160.
 DE
 XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KW cancer; contamination; biofilm; antibody; immune response.
 XX
 OS Aspergillus fumigatus.
 XX
 XX W0200286090-A2.
 PN
 PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013142.
 PF
 XX 23-APR-2001; 2001US-0285697P.
 PR 27-APR-2001; 2001US-0287066P.
 PR 05-JUN-2001; 2001US-0295890P.
 PR 09-JUL-2001; 2001US-0303899P.
 PR 31-AUG-2001; 2001US-0316362P.
 XX
 XX (ELIT-) ELITPA PHARM INC.
 XX
 XX Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM;
 PI WPI; 2003-093124/08.
 XX
 XX New purified or isolated nucleic acids of essential genes of Aspergillus
 PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 PT or for treating a non-infectious disease in a subject e.g. cancer.
 XX
 PS Disclosure; Page: 175pp; English.
 XX
 CC The invention relates to novel purified or isolated nucleic acids of

essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case of virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention

XX SQ Sequence 508 AA;

Query Match 78.3%; Score 1633; DB 6; Length 508;
 Best Local Similarity 78.6%; Pred. No. 1.2e-147;
 Matches 319; Conservative 35; Mismatches 36; Indels 16; Gaps 6;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAA-----SARVASVAVKAAVAPARQOVRGVKT 56
 DB 113 MASRGLPRALR-LAR-VAAP---RTVISALPRPALAKAATRAASTAP-----VRGVKT 162

QY 57 MDPAGHKEEVEHERADWPAEKLLDYFNKDTLALIGYSGQGHGGLNLDNGNLNIVGVKRN 116
 DB 163 IAFADSKETVYERADWPPEKLEQYFNKDTLALIGYSGQGHGGLNLDNGNLNIVGVKRD 222

QY 117 GKSMEDAIQDGVPGKGLFDVDEALSRGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 176
 DB 223 GASWEAIQDGVPGKGLFDVDEAVQKGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 282

QY 177 HGFSPVFKELTKVVEPTDVIDVILVAPKSGRTVRSIFREGRGINSFAVYQDVVTGKAKEK 236
 DB 283 HGFSPVFKELTKVDVDPKDVILVAPKSGRTVRLFREGRGINSFAVYQDVVTGKAKEK 342

QY 237 AVALGVAVSGSYLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERHSPSEAFN 296
 DB 343 AIAMGVAVSGSYLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERHSPSEAFN 402

QY 297 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWTPKPKDALKPVFNLYDSVKNGD 356
 DB 403 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWSSRFKDTLPKIFNELYDSVRDGT 462

QY 357 ERKRSLEYNQDYPYRYEAELEIRNLEIWRAGKR--SLRPNQK 400
 DB 463 ETKRSLEYNQDYPYRYEAELEIRNLEIWRAGKAVGSLRPNQK 508

RESULT 8
 ID ABJ25902 standard; protein; 388 AA.
 XX
 XX ABJ25902;
 AC
 XX
 DT 16-APR-2003 (first entry)
 XX
 XX Aspergillus fumigatus essential gene protein #560.
 DE
 XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KW cancer; contamination; biofilm; antibody; immune response.

CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case of virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of *Aspergillus fumigatus* of the invention
 XX
 SQ Sequence 500 AA;
 Query Match 76.9%; Score 1604; DB 6; Length 500;
 Best Local Similarity 78.7%; Pred. No. 6.9e-145;
 Matches 311; Conservative 35; Mismatches 35; Indels 14; Gaps 5;
 QY 1 MAARNCTKALRPLARQLATPAVQRRRTFVAASA-----SAVRASVAVKAAVAPARQOVRGVKT 56
 DB 113 MASRGLPRALR-LAR-VAAP-----RTVISALPRPALAKAATRAAATAP-----VRGVKT 162
 QY 57 MDPAGHKEEVEVHERADWPAEKLLDYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVGRKN 116
 DB 163 IAFADSKSETVYERADWPREKLOEYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVGRKD 222
 QY 117 GKSWEDAIQDGWPGKLVDFVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLIFS 176
 DB 223 GASKEAIQDGWIPGKLVDFLDEAVQGTIVMNLSDAAQSETWPTLKLITKGKTLIFS 282
 QY 177 HGFSVPFKDLTKVEVPTDNDVILVAPKSGRTVRSLEFRGGINSSPAVYQDVTGKAKEK 236
 DB 283 HGFSVPFKDLTKVDVDPKDVILVAPKSGRTVRLFRGGINSSPAVYQDVTGKAKEK 342
 QY 237 AVALGVAVGSGLYYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 296
 DB 343 AIAMGVAVGSGLYYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 402
 QY 297 ETVEEATQSLYPLIGAGMDWDFACSTTARRGAIDWTPKFDALKPVENNLYDSVKNGD 356
 DB 403 ETVEEATQSLYPLIGAGMDWMAACSTTARRGAIDWSSRFKDTLPKFIFNELYDSVRDGT 462
 QY 357 ERKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK 391
 DB 463 ETKRSLEYNQKDYREKYEKEMQDIRDLEIWRAGK 497
 RESULT 10
 AAU15089
 ID AAU15089 standard; protein; 400 AA.
 XX
 AC AAU15089;
 XX
 XX 04-DEC-2001 (first entry)
 XX
 XX Protein encoded by *C. albicans* essential gene *CaYLR355C* (ILV5).
 DE
 XX Gene identification; essential gene; GRACE; pathogenic fungus;
 KW gene replacement and conditional expression; fungal infection.
 XX
 XX Candida albicans.
 XX
 XX WO200160975-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US005551.
 XX
 XX 18-FEB-2000; 2000US-0183534P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 XX Roemer T, Jiang B, Boone C, Bussey H;
 XX
 XX WPI; 2001-489080/53.
 XX
 XX N-PSDB; AAS23417.
 DR

XX Identifying genes essential to fungal metabolisms and identifying
 PT potential therapeutic agents that target these genes.
 XX
 XX Claim 43; Page 222-223; 324pp; English.
 XX
 CC The present invention relates to novel methods for constructing fungal
 CC strains useful for identification and validation of gene products as
 CC targets for therapeutic agents, for creating a collection of identified
 CC essential genes, and screening assays for the discovery of new drugs. The
 CC invention provides the GRACE (gene replacement and conditional
 CC expression) method for the construction of mutant organisms referred to
 CC as GRACE strains of the organism. The invention can be applied to any
 CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,
 CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful
 CC to identify agents that may be used in the treatment of fungal
 CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*
 CC essential genes
 XX
 SQ Sequence 400 AA;
 Query Match 73.8%; Score 1539.5; DB 4; Length 400;
 Best Local Similarity 73.1%; Pred. No. 7.9e-139;
 Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;
 QY 1 MAARNCTKALRPLARQLATPAVQRRRTFVAASA-----VRASVAVKAAVAPARQOVRGVKT 56
 DB 1 MSPRTTSMRMARLATAKAT--LSKRTFSLANATTTRYTAASSAAKAMTPTT--SIRGVKT 56
 QY 57 MDPAGHKEEVEVHERADWPAEKLLDYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVGRKN 116
 DB 57 INFGGTEEVVHERADWPKERLLDYFNKDTFALIGYSGGQGLNLRDGLNIVGVGRK- 115
 QY 117 GKSWEDAIQDGWPGKLVDFVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLIFS 176
 DB 116 GSSWEAAVEDGWVGENLFEVDEAISRGTTIMDLSDDAAQSETWPHIKPOLTEGKTLIFS 175
 QY 177 HGFSVPFKDLTKVEVPTDNDVILVAPKSGRTVRSLEFRGGINSSPAVYQDVTGKAKEK 236
 DB 176 HGFSVPFKDLTKVEPPSNIDVILAAPKSGRTVRSLEFRGGINSSPAVYQDVTGKAKEK 235
 QY 237 AVALGVAVGSGLYYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 296
 DB 236 AIAMGVAVGSGLYYETTFEKEVSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFN 295
 QY 297 ETVEEATQSLYPLIGAGMDWDFACSTTARRGAIDWTPKFDALKPVENNLYDSVKNGD 356
 DB 296 ETVEEATQSLYPLIGAGMDWYDADCTTARRGALDWPYFFKDALXKPVFEELYESVKNGS 355
 QY 357 ERKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
 DB 356 ETKRSLEFNRSYDKERLEELQTIIRNMEIWRVGEVRLRPNQ 400
 RESULT 11
 ABP73238
 ID ABP73238 standard; protein; 400 AA.
 XX
 AC ABP73238;
 XX
 XX 30-JAN-2003 (first entry)
 XX
 XX Candida albicans essential protein SEQ ID NO 7075.
 DE
 XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 XX proliferation; Candida albicans; fungicide; antifungal.
 XX
 XX Candida 'albicans'.
 OS
 XX WO200253728-A2.
 XX
 XX 11-JUL-2002.
 PD

Best Local Similarity 73.6%; Pred. No. 7.4e-136;

Best Local Similarity 73.6%; Pred. No. 7.4e-136;

the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

68.2%;	Score	1423.5;	DB	7;	Length	409;	
Best Local Similarity	70.2%;	Fred.	No.	1.2e-127;			
Matches	278;	Conservative	47;	Mismatches	127;		
				Indels	9;	Gaps	3;

QY	3	ARNCTKALRPLARQLATPAVORRTF-VAAASAVRASVAVKAVAPARQQVRGVKTWDFAG	61
Db	4	SRASSNALKQALKSTASQVARRSYSLSGAAPAAMATRLGA-----TRGIKTLDFAG	57
QY	62	HKEEVHERADWPAPKLLDYFKNDTIALIIGYSQGHGGLNLRNGNLNVIVGVRKNKGWSB	121
Db	58	TKEVVYERADWPLDKLDQDYFNKDITLAMIIGYSQGHSGLNARDNLGLKVIIVGRVKGESWK	117
QY	122	DAIQDQWPGKGNLFDDVEATSRGTIVNNLSDDAQSETTPHIKPQITKGTLYFSHGFSP	181
Db	118	QAQEDGWVPGETLFDIPALNKGTIIINWLSDAAQSQTWNIEAPLTIKGKTLFAHGFVS	177
QY	182	VFKOLTKEYEPTDVVDVILVAPKSGSRTVRSFLPREGRGINSSFAYQDVTGKAKEKAAVALG	241
Db	178	VVKEDTHVIPPKDVDVILVAPKSGSRTVRTLFLLEGRCINSSIAVYQDVTGHAKKAAVALG	237
QY	242	VAVGSGLYLETTFPEKVYSDLYGSRGCLMGGIHCMFLAOYEVLBERGHSPSEAFNETVSE	301
Db	238	IAVSGSLYLETTFPEKVYSDLYGSRGVLMGGIQMFLAOYEVLIRKNGHSPSEAFNETVSE	297
QY	302	ATQSLYPLIGHGMDWMFDCSTTARRGAIIDWTVPKKFDALKPFPNNLYDSVKNGDERKKS	361
Db	298	ATQSLFPLLIGKYGMVYNACSTTARRGALDWAPKFKEANLPVEALYNSVRDGETRS	357
QY	362	LEYNSQPYRRERYAEADDEINLEIWRAK--RSLR	395
Db	358	LEFNSRKTYREDLOKELDEDINOBIWRAGTKTVRGLR	393

RESULT 15
ABU20976
ID ABU20976 standard; protein; 347 AA.
XX
XX AC ABU20976;
XX
XX
XX DT
XX DT 19-JUN-2003 (first entry)
XX
XX
XX DE Protein encoded by Prokaryotic essential gene #6503.

KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX	
XX	
OS	Bacteroides fragilis.
XX	
XX	WO200277183-A2.
XX	
XX	03-OCT-2002.
XX	
XX	21-MAR-2002; 2002WO-US009107.
XX	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
XX	(ELIT-) ELITRA PHARM INC.
XX	
XX	Wang L, Zamudio C, Malone C, Zyskind JW;
PPI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX	
XX	WPI; 2003-029926/02.
DR	N-PSDB; ACA24846.
DR	

for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of the 5213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct_sequences](http://www.int/pub/published/pct_sequences)

[illegible]

Search completed: March 22, 2006, 15:27:06
Job time : 115.954 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on:

March 22, 2006, 15:21:02 ; Search time 113.517 Seconds
(without alignments)
1528.885 Million cell updates/sec

Title: US-10-797-248a-2

Perfect score: 2071

Sequence: 1 MLRTQARLLCNSRVITAKR.....RNMEIKVGKVKLRPENQ 395

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1940s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	6 ABR64304	ABR64304 Acetohydr
2	2071	100.0	395	7 ADK64188	ADK64188 Disease t
3	1667	80.5	400	4 AAU15089	AAU15089 Protein e
4	1667	80.5	400	5 ABP73238	ABP73238 Candida a
5	1508.5	72.8	400	6 ABR64305	ABR64305 Acetohydr
6	1507	72.8	400	6 ABR64306	ABR64306 Acetohydr
7	1507	72.8	400	9 ADV16807	ADV16807 M grisea
8	1503	72.6	402	6 ABR64303	ABR64303 Acetohydr
9	1487.5	71.8	396	6 ABJ26477	ABJ26477 Aspergill
10	1487.5	71.8	508	6 ABJ26502	ABJ26502 Aspergill
11	1482.5	70.6	388	6 ABJ25902	ABJ25902 Aspergill
12	1462.5	70.6	500	6 ABJ25877	ABJ25877 Aspergill
13	1448.5	69.9	403	9 ADV16810	ADV16810 M grani
14	1392.5	67.2	409	7 ADB70124	ADB70124 C. neofo
15	1099.5	53.1	347	6 ABU20976	ABU20976 Protein e
16	495	23.9	332	4 AAB96356	AAB96356 Putative
17	470	22.7	337	6 ABU24174	ABU24174 Protein e
18	465	22.5	331	5 ABB48168	ABB48168 Listeria
19	465	22.5	331	6 ABU32456	ABU32456 Protein e
20	461	22.3	342	4 AAU01250	AAU01250 B. subtil
21	458.5	22.1	334	4 AAG81458	AAG81458 S. epide
22	458.5	22.1	334	6 ABU42920	ABU42920 Protein e
23	458.5	22.1	339	5 ABP39068	ABP39068 Staphyloc
24	458.5	22.1	339	8 ADS07053	ADS07053 Staphyloc

25	457.5	22.1	326	7 ADM26226	Adm26226 Hyperther
26	450.5	21.8	336	6 ABU18526	Abu18526 Protein e
27	441.5	21.3	328	4 AAU34233	Aau34233 Staphyloc
28	441.5	21.3	334	4 AAU36568	Aau36568 Staphyloc
29	441.5	21.3	334	6 ABU16517	Abu16517 Protein e
30	439.5	21.2	334	6 ABU43732	Abu43732 Protein e
31	436	21.1	369	6 ABP77403	Abp77403 N. gonorr
32	435.5	21.0	591	5 ABB92723	Abb92723 Herbicida
33	435.5	21.0	591	8 ADT55519	Adt55519 Plant pol
34	435	21.0	340	6 ABU44602	Abu44602 Protein e
35	434.5	21.0	339	6 ABM70896	Abm70896 Staphyloc
36	433.5	20.9	337	6 ABU38085	Abu38085 Protein e
37	433.5	20.9	337	8 ADP08317	Adp08317 Neisseria
38	433.5	20.9	337	9 AEB19104	Aeb19104 Neisseria
39	433	20.9	586	2 AAY26182	Aay26182 Soybean a
40	432	20.9	331	6 ABU25629	Abu25629 Protein e
41	431.5	20.8	549	3 AAG26356	Aag26356 Arabidops
42	431	20.8	340	4 AAU37780	Aau37780 Streptoco
43	431	20.8	340	4 AAU38003	Aau38003 Streptoco
44	431	20.8	340	6 ABU00804	Abu00804 S. pneumo
45	431	20.8	340	6 ABU45897	Abu45897 Protein e

ALIGNMENTS

RESULT 1

ABR64304

ID ABR64304 standard; protein; 395 AA.

XX ABR64304;

XX 16-SEP-2003 (first entry)

DE Acetohydroxyacid isomeroreductase.

XX Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase;

XX yeast.

OS Saccharomyces cerevisiae.

XX FR2829363-A1.

XX 14-MAR-2003.

XX 10-SEP-2001; 2001FR-00011689.

XX 10-SEP-2001; 2001FR-00011689.

XX (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;

XX WPI; 2003-405775/39.

Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase.

XX Claim 2; Fig 1; 66pp; French.

The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention

XX Sequence 395 AA;

Query Match 100.0%; Score 2071; DB 6; Length 395;

Best Local Similarity 100.0%; Pred. No. 1.3e-186;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
DB 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGQGLNLRDGLNVIIGVRKDGASWKAIAED 120
DB 61 YERADWPREKLLDYFKNDTFALIGYSGQYGQGLNLRDGLNVIIGVRKDGASWKAIAED 120
QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPKDL 180
DB 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPKDL 180
QY 181 THVEPPKDLVDVILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
DB 181 THVEPPKDLVDVILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
QY 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
DB 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
QY 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
DB 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
QY 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
DB 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
RESULT 2
ADK64188
ID ADK64188 standard; protein; 395 AA.
AC ADK64188;
XX
DT 05-MAY-2004 (first entry)
DE Disease treating protein complex-derived protein #1281.
DE protein complex; drug target; diagnosis.
XX Unidentified.
XX EP1338608-A2.
XX
PD 27-AUG-2003.
PF 20-DEC-2002; 2002EP-00102902.
XX 20-DEC-2001; 2001EP-00130253.
XX (CELL-) CELLZONE AG.
XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
PI Michon A, Leutwein C, Rick J;
XX WPI; 2003-638460/61.
DR N-PSDB; ADK64189.
XX New proteins and protein complexes from eukaryotes, useful as targets in
PT drug screening, or in diagnosing or screening for the presence of a
PT disease or disorder, or a predisposition for developing a disease or
PT disorder in a subject.
XX Disclosure; SEQ ID NO 2561; 13pp; English.
XX
XX The invention relates to novel protein complexes comprising a first and a
CC second protein, or its derivative, fragment, homologue or variant. The
CC proteins are selected from given protein complexes, which are not defined
CC in the specification. The variants are encoded by nucleic acids that
CC hybridize to the nucleic acids encoding the proteins under low stringency

CC conditions. The protein complexes are useful as targets for an active
CC agent of a pharmaceutical. These protein complexes are particularly
CC useful as drug targets for the treatment or preventing of a disease or
CC disorder. The complexes and methods above are useful in diagnosing or
CC screening for the presence of a disease or disorder or a predisposition
CC for developing a disease or disorder in a subject. These are also useful
CC in screening for a drug for treatment or prevention of a disease or
CC disorder. The molecule that modulates the amount, activity or protein
CC components of the complex is useful for the manufacture of a medicament
CC for the treatment or prevention of a disease or disorder. This sequence
CC corresponds to a protein of the invention. (Note: the sequence data for
CC this patent did not form part of the printed specification but was
CC obtained from the EPO in electronic format).
XX Sequence 395 AA;
SQ
Query Match 100.0%; Score 2071; DB 7; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.3e-186;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
DB 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGQGLNLRDGLNVIIGVRKDGASWKAIAED 120
DB 61 YERADWPREKLLDYFKNDTFALIGYSGQYGQGLNLRDGLNVIIGVRKDGASWKAIAED 120
QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPKDL 180
DB 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPKDL 180
QY 181 THVEPPKDLVDVILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
DB 181 THVEPPKDLVDVILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
QY 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
DB 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
QY 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
DB 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
QY 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
DB 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
RESULT 3
AAU15089
ID AAU15089 standard; protein; 400 AA.
XX
AC AAU15089;
XX
DT 04-DEC-2001 (first entry)
DE Protein encoded by C. albicans essential gene CAYLR355C (ILV5).
XX
XX Gene identification; essential gene; GRACE; pathogenic fungus;
KW gene replacement and conditional expression; fungal infection.
XX Candida albicans.
XX
XX WO200160975-A2.
PN
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005551.
PF
XX 18-FEB-2000; 2000US-0183534P.
PR
XX (ELIT-) ELITRA PHARM INC.
PA

XX Roemer T, Jiang B, Boone C, Bussey H;
 XX WPI; 2001-489080/53.
 DR N-PSDB; AAS23417.
 XX
 XX Identifying genes essential to fungal metabolisms and identifying
 PT potential therapeutic agents that target these genes.
 PT
 XX Claim 43; Page 222-223; 324pp; English.
 XX
 XX The present invention relates to novel methods for constructing fungal
 CC strains useful for identification and validation of gene products as
 CC targets for therapeutic agents, for creating a collection of identified
 CC essential genes, and screening assays for the discovery of new drugs. The
 CC invention provides the GRACE (gene replacement and conditional
 CC expression) method for the construction of mutant organisms referred to
 CC as GRACE strains of the organism. The invention can be applied to any
 CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,
 CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful
 CC to identify agents that may be used in the treatment of fungal
 CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*
 CC essential genes
 XX
 XX Sequence 400 AA;
 SQ
 Query Match 80.5%; Score 1667; DB 4; Length 400;
 Best Local Similarity 79.1%; Pred. No. 2.2e-148;
 Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;
 QY 3 RTQARL--ICNSRVITAKTFAL---ATRAAAYSRAARFVKPMITRGLKQINFGTV 57
 DB 4 RTTSMRVARLATAKATLSKRTFSLANATRYTAASAAKAMTPTITSIRGVKTINGGTE 63
 QY 58 ETYVERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRKDGASWAA 117
 DB 64 EVVHERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRK-GSSWEA 122
 QY 118 IEDGWVPGKDLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTFSHGSPVF 177
 DB 123 VEDGWVPGENLFEVDEAISRGTIIMDLLSDAAQSETWFWHIKPOLTEGKTLTFSHGSPVF 182
 QY 178 KOLTHVEPPKDLVDVILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHEKAQALAVA 237
 DB 183 KOLTHVEPPSNIDVILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHEKAIAAIA 242
 QY 238 IGSQVYVQTTFERVNSDLXGERCLMGGIHGMFLAQYDVLRENGHSPSAFNETVEEAT 297
 DB 243 IGSQVYVQTTFERVNSDLXGERCLMGGIHGMFLAQYEVIRENGHTPSEAFNETVEEAT 302
 QY 298 QSLYPLIGKYGMDYWDACSTTARRGALDWYPIPKNAKPFVDLYESTKNGTETKRSLE 357
 DB 303 QSLYPLIGKYGMDYWDACSTTARRGALDWYPRFKDALKVPFEELYESVNGSETKRSLE 362
 QY 358 FNSQPDYREKLEKDLTIRNWEIKWQKVRKLRPENQ 395
 DB 363 FNSRSDYKERLEELQIRNWEIKWQKVRKLRPENQ 400
 RESULT 4
 ABP73238
 ID ABP73238 standard; protein; 400 AA.
 XX
 XX AC ABP73238;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 XX *Candida albicans* essential protein SEQ ID NO 7075.
 DE
 XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; *Candida albicans*; fungicide; antifungal.
 XX

OS *Candida albicans*.
 PN WO200253728-A2.
 XX
 PD 11-JUL-2002.
 XX
 XX 26-DEC-2001; 2001WO-US049486.
 XX
 XX 29-DEC-2000; 2000US-0259128P.
 PR 20-FEB-2001; 2001US-00792024.
 PR 22-AUG-2001; 2001US-0314050P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 PI WPI; 2002-566694/60.
 XX N-PSDB; ABZ31788.
 DR
 DR
 XX Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele of
 PT a gene and placing other allele of the gene under conditional expression.
 XX
 XX Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.
 XX
 XX The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthesis, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of *C. albicans* cells and for
 CC treating infection by *C. albicans*. The present sequence is that of an
 CC essential *Candida albicans* protein used in the method of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office
 XX
 XX Sequence 400 AA;
 SQ
 Query Match 80.5%; Score 1667; DB 5; Length 400;
 Best Local Similarity 79.1%; Pred. No. 2.2e-148;
 Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;
 QY 3 RTQARL--ICNSRVITAKTFAL---ATRAAAYSRAARFVKPMITRGLKQINFGTV 57
 DB 4 RTTSMRVARLATAKATLSKRTFSLANATRYTAASAAKAMTPTITSIRGVKTINGGTE 63
 QY 58 ETYVERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRKDGASWAA 117
 DB 64 EVVHERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRK-GSSWEA 122
 QY 118 IEDGWVPGKDLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTFSHGSPVF 177
 DB 123 VEDGWVPGENLFEVDEAISRGTIIMDLLSDAAQSETWFWHIKPOLTEGKTLTFSHGSPVF 182
 QY 178 KOLTHVEPPKDLVDVILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHEKAQALAVA 237
 DB 183 KOLTHVEPPSNIDVILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHEKAIAAIA 242


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QY 238 IGSYVYQTTFFREVNSDLYGERGCLMGHFLAQYDVLRENGHSPSEAFNETVEAT 297
Db 243 IGSYVYKTTFFREVNSDLYGERGCLMGHFLAQYEVLRNGHTPSEAFNETVEAT 302
QY 298 QSLYPLIGKYGMDYDACSTTARRGALDWPYPIFKALKQVFDLYESTKNGTETKRSLE 357
Db 303 QSLYPLIGKYGMDYDACSTTARRGALDWPYPRFDALKEVPELYESVKNGETKRSLE 362
QY 358 FNSQPDYREKLEKELDTIRNMEIWKVGEVKRLRPENQ 395
Db 363 FNSRSDYKERLEBELQTI RNMEIWRVGEVKRLRPENQ 400

RESULT 5
ABR64305
ID ABR64305 standard; protein; 400 AA.
XX
AC ABR64305;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductase.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Neurospora crassa.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX
PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
PS Claim 2; Fig 1; 66pp; French.
XX
CC The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase. (I) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 400 AA;

Query Match 72.8%; Score 1508.5; DB 6; Length 400;
Best Local Similarity 73.6%; Pred. No. 2.1e-133;
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;

QY 4 TOARLICNSRVITA---KRTF---ALATRAA---AYSRPAARFVKPMITRGLKQINFG 54
Db 7 TKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQV-----RGVKTMDFA 60
QY 55 GTVETVYERADWPREKLLDYFKNDTFTALIGYSGQYGGQGLNLRDNGLNVIIGVRKDGASW 114
Db 61 GHKEEYERADWPAREKLLDYFKNDTFTALIGYSGQYGGQGLNLRDNGLNVIIGVRKNGKSW 120
QY 115 KAAIEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKLTLYFSHGFS 174
Db 121 EDRIQGWVPGKNLFDVDEAISRTIVMNLSDAAQSETWPHIKPQITGKLTLYFSHGFS 180
QY 175 PVFKDLTHVEPPKOLDVILVAPKSGRTVRSLFKEGRGINSSYAVWVNDVTGKAHEKAQAL 234
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Db 181 PVFKDLTKVEVPTDQVDVILVAPKSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL 240
QY 235 AVAIGSYVYQTTFFREVNSDLYGERGCLMGHFLAQYDVLRENGHSPSEAFNETVE 294
Db 241 GVAVSGYLYETTFEKEVYSDLYGERGCLMGHFLAQYEVLRNGHSPSEAFNETVE 300
QY 295 EATQSLYPLIGKYGMDYDACSTTARRGALDWPYPIFKALKQVFDLYESTKNGTETKR 354
Db 301 EATQSLYPLIGAGMDWDFDACSTTARRGALDWTFFKDALPVPFNLYDSVKNGDERKR 360
QY 355 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVKRLRPENQ 395
Db 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399

RESULT 6
ABR64306
ID ABR64306 standard; protein; 400 AA.
XX
AC ABR64306;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductas #2.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Magnaporthe grisea.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX
DR N-PSDB; ACC80185, ACC80186.
XX
PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
PS Disclosure; Page 57-58; 66pp; French.
XX
CC The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase. (I) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 400 AA;

Query Match 72.8%; Score 1507; DB 6; Length 400;
Best Local Similarity 73.2%; Pred. No. 2.9e-133;
Matches 289; Conservative 44; Mismatches 56; Indels 6; Gaps 3;

QY 2 LHTQARLICNSRVITAKRTFTALATRAAAYSRPAARFVKP-MITRGLKQINFGTVEIV 60
Db 10 LRPMAQL---ATPAVQRRTFVAASVMVRATRKAA--VAPTOQOIRGVKTMDFAGHKEQV 64
QY 61 YERADWPREKLLDYFKNDTFTALIGYSGQYGGQGLNLRDNGLNVIIGVRKDGASWKAALIED 120
Db 65 WERADWPREKLLDYFKNDTFTALIGYSGQYGGQGLNLRDNGLNVIIGVRKDGSKWDAVDQ 124
QY 121 GWVPKGNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKLTLYFSHGFSVPFKDL 180
```

Db 125 GWVFGKMLFEVDEALSGVTIMNLLSDAAQSETWPAKLPQITKGTLYFSGHSPVPKDL 184
 Qy 181 THVEPPKDLVDILVAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
 Db 185 TKVEVPTDVIDILCAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 244
 Qy 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNTEVEATQSL 300
 Db 245 GYLKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 304
 Qy 301 YPLIGKGMVMDYDACSTTARRGALDWYPIFKNALKPVDLYESTKNGTETKRSLEFNS 360
 Db 305 YPLIGANGMDWYEAACSTTARRGALDMSPRFKDALKPFVFNQLYDSVKGSETQSLDYS 364
 Qy 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395
 Db 365 QPDYREKYEAEEMBEIRNLEIWRAGKAVRSLRPENQ 399
 RESULT 7
 ADV16807
 ID ADV16807 standard; protein; 400 AA.
 XX AC ADV16807;
 XX DT 24-FEB-2005 (first entry)
 XX DE M grisea ketol-acid reductoisomerase ILV5 seqid 6.
 XX KW substrate inhibition; antibiotic; gene disruption;
 KW ketol-acid reductoisomerase; ILV5; enzyme.
 XX OS Magnaporthe grisea.
 XX PN WO2004104176-A2.
 XX PD 02-DEC-2004.
 XX PF 17-MAY-2004; 2004WO-US015404.
 XX PR 15-MAY-2003; 2003US-0470947P.
 XX PR 19-MAY-2003; 2003US-0471615P.
 XX PR 21-MAY-2003; 2003US-0472422P.
 XX PA (PARA-) PARADIGM GENETICS INC.
 XX PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC,
 PI Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;
 PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX WPI; 2005-021202/02.
 DR N-PSDB; ADV16805, ADV16806.
 XX Identifying a test compound as a candidate for an antibiotic comprises
 PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
 PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
 PT with a test compound.
 XX Claim 48; SEQ ID NO 6; 179pp; English.
 XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated

CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
 XX Sequence 400 AA;
 Qy 2 LRTQARALICNSRVITAKRTFALATRAAAYSRPAARFVKP-MITTRGLKQINFGGTVETV 60
 Db 10 LRPMARQL---ATPAVQRRITFVAASSMVRATKAA--VAPTQQOIRGVKTMDFAGHKEQV 64
 Qy 61 YERADWPREKLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVIIGVRKDGASWKAALIED 120
 Db 65 WERADWPKEKLEYLEYFKDDTLALIGYSGHGGHGLNLRDNLNGLNVIIGVRKDGSKWDAVQD 124
 Qy 121 GWVPGKMLFTVEDAIKRGSYVMNLLSDAAQSETWPAKLPQITKGTLYFSGHSPVPKDL 180
 Db 125 GWVPGKMLFEVDEALSGVTIMNLLSDAAQSETWPAKLPQITKGTLYFSGHSPVPKDL 184
 Qy 181 THVEPPKDLVDILVAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
 Db 185 TKVEVPTDVIDILCAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 244
 Qy 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNTEVEATQSL 300
 Db 245 GYLKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 304
 Qy 301 YPLIGKGMVMDYDACSTTARRGALDWYPIFKNALKPVDLYESTKNGTETKRSLEFNS 360
 Db 305 YPLIGANGMDWYEAACSTTARRGALDMSPRFKDALKPFVFNQLYDSVKGSETQSLDYS 364
 Qy 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395
 Db 365 QPDYREKYEAEEMBEIRNLEIWRAGKAVRSLRPENQ 399
 RESULT 8
 ABR64303
 ID ABR64303 standard; protein; 402 AA.
 XX AC ABR64303;
 XX DT 16-SEP-2003 (first entry)
 XX DE Acetohydroxyacid isomeroeductase #1.
 XX KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroeductase.
 XX OS Magnaporthe grisea.
 XX PN FR2829363-A1.
 XX PD 14-MAR-2003.
 XX PF 10-SEP-2001; 2001FR-00011689.
 XX PR 10-SEP-2001; 2001FR-00011689.
 XX PA (AVET) AVENTIS CROPS SCIENCE SA.
 XX PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX WPI; 2003-405775/39.
 XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
 PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroeductase.
 XX

PS Claim 2; Fig 1; 66pp; French.

XX The present invention relates to a method for controlling fungal disease

CC in crops by applying an inhibitor (I) of acetohydroxyacid

CC isomeroreductase. (I) are used for curative or preventative treatment of

CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or

CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used

CC to illustrate the invention

XX

SQ Sequence 402 AA;

Query Match 72.6%; Score 1503; DB 6; Length 402;

Best Local Similarity 72.9%; Pred. No. 7.1e-133;

Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;

QY 2 LRTQAARLINCNSRVITAKRTFALATRAAAYSRPAAREVKP-MITTRGLKQINFGGTVETV 60

DB 10 LRPWARGL---ATPAVQRSSFVAASSMVRATRXAA--VAPTQQIRGVKTMDFAGHKEQV 64

QY 61 YERADWPREKLDYFKNDTFALIGYSGQYGGQGLNLRDNGLVIIIGVRKDGASWKAIAED 120

DB 65 WERADWPREKLEFYKDDTLALIGYSGQGHGQGLNLRDNGLVIIIGVRKDGKSKDAVQD 124

QY 121 GWPGKNLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180

DB 125 GWPGKNLFTVEDAISRGTVIMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 184

QY 181 THVEPPKDLVDILVAPKSGSRTVRSIFKEGRGINSSYAVMNDVTGKAHEKAQALAVAIGS 240

DB 185 TKVEPPTDVIDLCAKSGSRTVRSIFKEGRGINSSYAVMNDVTGKAHEKAQALAVAIGS 244

QY 241 GYVQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVEEATQSL 300

DB 245 GYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNVEEATQSL 304

QY 301 YPLIGKYGMDYDACSTTARRGALDWPYIPFNKALKPVFODLYESTKNGTETKRSLEFNS 360

DB 305 YPLIGANGMDYACSTTARRGALDWPYIPFNKALKPVFODLYESTKNGTETKRSLEFNS 364

QY 361 QPDYREKLEKELDTIRNMEIWKVGEVKRLRPENQ 395

DB 365 QPDYREKYEAMEEIRNLEIWRAGKAVRSIRPENQ 399

RESULT 9

ABJ26477

ID ABJ26477 standard; protein; 396 AA.

AC ABJ26477;

XX

XX 16-APR-2003 (first entry)

DE Aspergillus fumigatus essential gene protein #1135.

XX

XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;

KW cancer; contamination; biofilm; antibody; immune response.

XX

OS Aspergillus fumigatus.

XX

XX WO200286090-A2.

PN

XX

XX 31-OCT-2002.

XX

XX 23-APR-2002; 2002WO-US013142.

XX

XX 27-APR-2001; 2001US-0285697P.

PR

XX 23-APR-2001; 2001US-0287066P.

PR

XX 05-JUN-2001; 2001US-0295890P.

PR

XX 09-JUL-2001; 2001US-0303899P.

PR

XX 31-AUG-2001; 2001US-0316362P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;

XX WPI; 2003-093124/08.

DR

XX New purified or isolated nucleic acids of essential genes of Aspergillus

PT fumigatus, useful for treating or preventing infections by A. fumigatus,

PT or for treating a non-infectious disease in a subject e.g. cancer.

XX

PS Disclosure; Page: 175pp; English.

XX

CC The invention relates to novel purified or isolated nucleic acids of

CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of

CC the invention are used to treat or prevent infections by a pathogenic

CC organism such as A. fumigatus, to treat a non-infectious disease in a

CC subject (e.g. cancer), to prevent or contain contamination of an object

CC by A. fumigatus, or to prevent or inhibit formation on a surface of a

CC biofilm comprising A. fumigatus. The polynucleotides are useful for

CC expressing recombinant protein for characterisation, screening or

CC therapeutic use, as markers for host tissues in which the pathogenic

CC organisms invade or reside, for comparing with the DNA sequence of A.

CC fumigatus to identify duplicated genes or paralogues having the same or

CC similar biochemical activity and/or function, for comparing with DNA

CC sequences of other related or distant pathogenic organisms to identify

CC potential orthologous essential or virulence genes, for selecting and

CC making oligomers for attachment to a nucleic acid array for examination

CC of expression patterns, for raising anti-protein antibodies, as an

CC antigen to raise anti-DNA antibodies or to elicit another immune

CC response, and for identifying polynucleotides encoding the other protein

CC with which binding occurs or to identify inhibitors of the binding

CC interaction. The polypeptides may be used to raise antibodies or to

CC elicit immune response, as a reagent in assays designed to quantitatively

CC determine levels of the protein in biological fluids, as a marker for

CC host tissues in which pathogenic organism invade or reside, and to

CC isolate correlative receptors or ligands in the case of virulence

CC factors. This sequence represents a protein of one of the essential genes

CC of Aspergillus fumigatus of the invention

XX

SQ Sequence 396 AA;

Query Match 71.8%; Score 1487.5; DB 6; Length 396;

Best Local Similarity 71.6%; Pred. No. 2e-131;

Matches 280; Conservative 46; Mismatches 62; Indels 3; Gaps 1;

QY 5 QAARLICNSRVITAKRTFALATRAAAYSRPAARFKVPMITTRGLKQINFGGTVETVYERA 64

DB 8 RALRL---ARVAAPRTVISALPRPALAKAATRVAASTAPVRGVKTIAPADSKETVYERA 64

QY 65 DWPREKLDYFKNDTFALIGYSGQYGGQGLNLRDNGLVIIIGVRKDGASWKAIAEDGWVP 124

DB 65 DWPREKLDYFKNDTFALIGYSGQYGGQGLNLRDNGLVIIIGVRKDGASWKAIAEDGWVP 124

QY 125 GKNLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDLTHVE 184

DB 125 GKNLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDLTHVE 184

QY 185 PPKDLVDILVAPKSGSRTVRSIFKEGRGINSSYAVMNDVTGKAHEKAQALAVAIGSYVY 244

DB 185 VPKDQDVLVAPKSGSRTVRSIFKEGRGINSSYAVMNDVTGKAHEKAQALAVAIGSYVY 244

QY 245 QTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVEEATQSLYPLI 304

DB 245 ETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNVEEATQSLYPLI 304

QY 305 GKYGMDYDACSTTARRGALDWPYIPFNKALKPVFODLYESTKNGTETKRSLEFNSQDPY 364

DB 305 GANGMDYACSTTARRGALDWPYIPFNKALKPVFODLYESTKNGTETKRSLEFNSQDPY 364

QY 365 REKLEKELDTIRNMEIWKVGEVKRLRPENQ 395

DB 365 REKYEKEMQDIRDLEIWRAGKAVGSLRPENQ 395

RESULT 10

QY 5 QAAALICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTTRGLKQINFGTIVETVYERA 64

QY 305 GKYGMDYDASTTARRGALDWDYDFIKNALKPVFDLYSTVXNGTETKRSLEFNSQPDY 364
 DB 417 GANGMDWYAACTTARRGALDWSRRFKDTLKPIFNELYDSVRDGTETKRSLEFNSQDY 476
 QY 365 REKLEKELDTIRNMEIKVQKEVR 388
 DB 477 REKYEKEMQDINDLEIWRAGKAVR 500

RESULT 13
 ADV16810
 ID ADV16810 standard; protein; 403 AA.

XX AC ADV16810;
 XX DT 24-FEB-2005 (first entry)
 XX DE M graminicola ketol-acid reductoisomerase KAR1 seqid 9.
 XX KW substrate inhibition; antibiotic; gene disruption;
 XX KW ketol-acid reductoisomerase; KAR1; enzyme.

XX OS Mycosphaerella graminicola.
 XX PN WO2004104176-A2.
 XX PD 02-DEC-2004.
 XX PF 17-MAY-2004; 2004WO-US015404.
 XX PR 15-MAY-2003; 2003US-0470947P.
 XX PR 19-MAY-2003; 2003US-0471615P.
 XX PR 21-MAY-2003; 2003US-0472242P.
 XX PA (PARA-) PARADIGM GENETICS INC.

XX PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
 PI Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;
 PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX WPI; 2005-021202/02.
 XX DR N-PSDB; ADV16802, ADV16808, ADV16809.
 XX PS Claim 50; SEQ ID NO 9; 179pp; English.

XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
 CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of *Mycosphaerella graminicola* ketol-acid reductoisomerase KAR1.
 XX Sequence 403 AA;

Query Match 69.9%; Score 1448.5; DB 9; Length 403;
 Best Local Similarity 72.0%; Pred. No. 1e-127;

Matches 275; Conservative 41; Mismatches 57; Indels 9; Gaps 2;
 QY 19 KRTFALATRAAAYSRPAARFVKPMITT-----RGLKQINFGGTVETVYERADWPREKLL 72
 DB 24 QRSFVAANA---SRPSLVPAQKAVTSAFVQOVRGAKTVDFAGDKVKVFERDDHPREKLL 80
 QY 73 DYFKDTPFALIGYSGQYGGGLNLRDNLNVIIGVRKDGASWKAIAIDGWVPGNLFVTS 132
 DB 81 EYFKNDTLALIGYSGQYGGGLNLRDNLNVIIGVRKDGASWKAIAIDGWVPGNLFVTS 140
 QY 133 DAIRKGSVVMNLLSDAAQSETWPAIKPLLTGKTKLYFSHGFSVPFKDLTHVEPPKDLDDVI 192
 DB 141 TAICKGTIIWNLLSDAAQSETWPHIKPLMTKTKLYFSHGFSVPFKDQTKVEVPTDIDVI 200
 QY 193 LVAPKSGRTVRSIFKEGRGINSYAYVNDVTGKAHEKAQALAVAIGSGYVYQTTFFREV 252
 DB 201 LVAPKSGRTVRTLFEKGRGINSIAIFQDVTGKAEEKATGALGVAGSGYWKTTFFKEV 260
 QY 253 NSDLYGERGCLMGHIGMFLAQYDVLRENGHSSEAFNETVEEATQSLYPLIGKGMMDYM 312
 DB 261 YSDLYGERGCLMGHIGMFLAQYEVFLERGRHSSEAFNETVEEATQSLYPLIGKGMMDYM 320
 QY 313 YDASTTTARRGALDWDYPIFKNALKPVFDLYSTVXNGTETKRSLEFNSQPDYREKLEKEL 372
 DB 321 YEACSTTARRGALDWSKRFETLKPVEELYDSVKTQRTQRTMEYAGRKDYREAFREKEM 380
 QY 373 DTIRNMEIKVQKEVRKLRPEN 394
 DB 381 EEIRNLEIWRAGKAVRSRLEN 402

RESULT 14
 ADB70124
 ID ADB70124 standard; protein; 409 AA.
 XX AC ADB70124;
 XX DT 04-DEC-2003 (first entry)
 XX DE C. neoformans amino acid sequence SEQ ID NO:3168.
 XX KW fungicide; gene therapy; infection.
 XX OS Cryptococcus neoformans.
 XX PN WO2003052076-A2.
 XX PD 26-JUN-2003.
 XX PF 17-DEC-2002; 2002WO-US040225.
 XX PR 17-DEC-2001; 2001US-0341261P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Zamudio C, Eroshkin AM;
 XX WPI; 2003-533017/50.
 XX DR N-PSDB; ADB69041.
 XX PT New nucleic acid, useful for preparing a composition for treating an
 XX infection caused by *Cryptococcus neoformans*.
 XX Claim 9; SEQ ID NO 3168; 136pp; English.

XX The invention relates to a novel purified or isolated *Cryptococcus*
 CC neoformans nucleic acid molecule comprising a sequence encoding a
 CC polypeptide comprising a sequence not given in the specification. A
 CC polynucleotide of the invention has fungicide activity, and may have a
 CC use in gene therapy. The nucleic acid is useful for preparing a
 CC composition for treating an infection caused by *Cryptococcus neoformans*.
 CC The present sequence represents a C. neoformans sequence of the
 CC invention. Note: The sequence data for this patent is not represented in

CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX	
SQ	Sequence 409 AA;
Query Match	67.2%; Score 1392.5; DB 7; Length 409;
Best Local Similarity	68.5%; Pred. No. 2.1e-122;
Matches 267;	Conservative 48; Mismatches 64; Indels 11; Gaps 2;
QY	2 LRTQARALICNSRVITAKRTTALATRAAAYSRPAARFVKPMITTRGLKQINFGGTETVTV 61
DB	15 LKSTASQV-----ARRSYLLSGAA-----PRAAMATRLGATRGKTLDPAGTKEVVY 63
QY	62 ERADWPREKLDYFKNDTFALIGYSGQYGGQGLNDRNGLNVIIVKRGKAGSAAIAEDG 121
DB	64 ERADWPLDKLDYFKNDTFLAMIGYSGQGHGQSLNARDNGLKVIIVGRKGESWKQAQEDG 123
QY	122 WVPKGNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPELLTKTKTLYFSGHSPVPFKDLT 181
DB	124 WVPGETLFDIPEAINKGTITMNLSDAAQSQTNWNEAPLTKTKTLYFAHGFSSVYKEDT 183
QY	182 HVBPFPKDLVDILVAPKSGRTVRSFLFKEGRGINSYAVMNDVTGKAHEKAQALVAIGSG 241
DB	184 HVIPPKDDVDILVAPKSGRTVTLFLEGRGINSYAVYQDVTGHAKAVALGIAVSG 243
QY	242 YVQTTFEREVNSDLYGERCLMGGIHGMFLAODYVLRNENGHSPSBAFNETVEEATOSLY 301
DB	244 YLYETTFEKEVYGDLYGERGLMGGIQGMFLAQYEVLRKNCHSPSBAFNETVEEATQSLF 303
QY	302 PLGKYGMDYMDACSTTARRGALDVPYIFKNALKPVQDLYESTKNGTETKESLFSNQ 361
DB	304 PLGKYGMDYMNACSTTARRGALDWPAPKEANLPVFEALYNSVRDGETRSLSFNSR 363
QY	362 PDYREKLEKELDTIRNMEIKVGEVRKLR 391
DB	364 KTYREDLQKELDEIDNQEIWRACKTVRGLR 393
RESULT 15	
ABU20976	
ID	ABU20976 standard; protein; 347 AA.
XX	
AC	ABU20976;
DT	19-JUN-2003 (first entry)
DE	Protein encoded by prokaryotic essential gene #6503.
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW	Bacteroides fragilis.
OS	
XX	WO200277183-A2.
PN	
PD	03-OCT-2002.
XX	
PF	21-MAR-2002; 2002WO-US0009107.
PR	
XX	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
XX	
PI	Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zyskind JW;
FI	Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX	
DR	WPI; 2003-029926/02.
DR	N-PSDB; ACA24846.
XX	
PT	New antisense nucleic acids, useful for identifying proteins or screening

PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 48900; 1766pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-required gene or its gene product lies
CC	or a gene on which the test compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than S. aureus, S. typhimurium,
CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pat_sequences
XX	
SQ	Sequence 347 AA;
Query Match	53.1%; Score 1099.5; DB 6; Length 347;
Best Local Similarity	59.4%; Pred. No. 8.2e-95;
Matches 206;	Conservative 53; Mismatches 87; Indels 1; Gaps 1;
QY	48 LKQINFGGTETVTERADWPREKLDYFKNDTFALIGYSGQYGGQGLNDRNGLNVIIVG 107
DB	1 MAQLNFGGVTVENVTRREEPFLEKAREVLKNETIIVIGYGVQGGOSLNRDNGFNVIIVG- 59
QY	108 RDXGASWKAALIEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGRTL 167
DB	60 QRPKTYEKAVADGWVPGTTLFGEACENGTIIMCLLSDAAVMSVWPTIKPVLTKAGKAL 119
QY	168 YFSGHGFSPVFKDLTHVEPPKDLVILVAPKSGRTVRSFLFKEGRGINSYAVMNDVTGKA 227
DB	120 YFSGHGFALTWSDRGTGVVPQKIDIVIMVAPKSGTSLRTMFLGRLGINSYAIYQDATGRA 179
QY	228 HEKAQALVAIGSYGVYQTTTFEREVNSDLYGERCLMGGIHGMFLAODYVLRNENGHSPSE 287
DB	180 MERTIALGIGVSGYLFTTFVREATSDLTGERGSLMGAIQGLLLAQYEVLRNENGHTPSE 239
QY	288 AFNETVEEATOSLYPLIGKYGMDYMDACSTTARRGALDWPYIFKNALKPVQDLYESTK 347
DB	240 AFNETVEELTQSLMPLFAKNGMDWMYANCSTTAAQALDWMGPFHDAIKPVQKLYNSVK 299
QY	348 NGTETKRSLEFNSQPDYREKLEKELDTIRNMEIKVGEVRKLRPEN 394
DB	300 TGNEAQISIDNSKPDYREKLEKELKALRESEWQTAIVTVRKLKLRPEN 346
Search completed: March 22, 2006, 15:27:05	
Job time : 115.517 secs	